

GenCore version 5.1.9  
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OM nucleic - nucleic search, using SW model

Run on: October 14, 2006, 12:40:35 ; Search time 13047 Seconds  
(without alignments)  
12251.650 Million cell updates/sec

Title: US-10-667-289-1  
Perfect score: 2857.4  
Sequence: 1 gctgtacggagattccatctg.....gctctgaaaaaaaaaaaaa 2859

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues  
Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
EST:  
1: gb\_est1:  
2: gb\_est3:  
3: gb\_est4:  
4: gb\_est5:  
5: gb\_est6:  
6: gb\_est7:  
7: gb\_est8:  
8: gb\_est9:  
9: gb\_est10:  
10: gb\_est11:  
11: gb\_est12:  
12: gb\_est13:  
13: gb\_est14:  
14: gb\_est15:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	589.6	20.6	651	14	AG176412 Pan trogl
2	562.4	19.7	757	7	BF211696
3	522.2	18.3	842	3	BF183992
4	501.8	17.6	583	3	BP282008
5	499.6	17.5	602	5	CD708943
6	488.4	17.1	628	14	AG154727
7	488.4	17.1	754	7	BF210400
8	482.6	16.9	917	7	BF238439
9	474.2	16.6	820	7	BF209716
10	448.8	15.7	823	7	BF238869
11	428	15.0	825	12	CC496590
12	424.8	14.9	916	3	BQ228535
13	353	12.4	513	7	BF239183
14	345.6	12.1	720	4	CB429984
15	316.2	11.1	540	7	BF212748
16	268.2	9.4	569	11	AG659233
17	252.4	8.8	438	11	AG678212
18	247.8	8.7	537	9	DB302402
19	246.2	8.6	870	11	AQ739907

C 20	245.8	8.6	635	14	DU666845	C1ufl-HI
C 21	243.8	8.5	557	11	AQ674674	HS_5485_B
C 22	243.6	8.5	946	11	AQ744276	HS_5508_A
C 23	243.2	8.5	539	7	AM500534	UT-HP-BN0
C 24	243.2	8.5	604	3	BM990713	UT-H-D10-
C 25	242.8	8.5	403	2	BG941633	BG941633 ax15d09.x
C 26	242.6	8.5	446	7	BE140949	MRO-HT006
C 27	242.6	8.5	1270	6	BC016019	Homo sapi
C 28	242	8.5	472	9	DA156998	DA156998
C 29	241.8	8.5	471	1	AI753904	AI753904
C 30	241.8	8.5	522	3	BU727226	BU727226
C 31	241.8	8.5	562	3	BQ638837	BQ638837
C 32	241.8	8.5	704	14	AG113471	AG113471
C 33	241.8	8.5	1336	2	BG674233	BG674233
C 34	241.8	8.5	2535	6	AF464877	AF464877
C 35	241.6	8.5	530	9	DA804882	DA804882
C 36	241.6	8.5	530	9	DA804558	DA804558
C 37	241.6	8.5	575	9	DB078664	DB078664
C 38	241.6	8.5	579	14	DU666109	DU666109
C 39	241.6	8.5	1159	2	BM465227	BM465227
C 40	241.4	8.4	757	3	BQ429569	BQ429569
C 41	241.2	8.4	5037	6	HSM807357	HSM807357
C 42	240.8	8.4	376	3	BM672810	BM672810
C 43	240.8	8.4	583	3	BP330444	BP330444
C 44	240.6	8.4	519	4	BX503510	BX503510
C 45	240.6	8.4	662	14	DU840715	DU840715

## ALIGNMENTS

RESULT 1  
AG176412  
LOCUS  
DEFINITION Pan troglodytes DNA, clone: RP43-047K09.T7, genomic survey  
ACCESSION AG176412  
VERSION AG176412.1 GI:16706092  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Pan.

REFERENCE  
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T., Totoki, Y., Watanabe, H., and Sakaki, Y.  
TITLE BAC end sequences of Library RPCI-43  
JOURNAL Unpublished  
AUTHORS 2 (bases 1 to 651)  
TITLE Direct Submision  
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: chimpanzee@sc.riken.go.jp, URL: http://hsp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
COMMENT Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the Red process and may have higher chance of clone tracking errors.

PRIMERS  
LIBRARY  
Vector : pBACE3.6  
R.site 1 : EcoRI  
R.site 2 : EcoRI  
Location/Qualifiers  
1..651  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/clone="RP43-047K09.T7"

## FEATURES

source

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/sex="male"
/cell_type="Lymphocytes"
/clone_lib="RPCT-43 Chimpanzee Male BAC Library"

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Query Match	20.6%	Score	589.6	DB	14	Length	651
Best Local Similarity	97.9%	Pred. No.	4.1e-79				
Matches	617	Conservative	1	Mismatches	10	Indels	2
						Gaps	2

QY	1747	TAATTTCTTGAGAAATTAACCTCAATTTAAATCAAGAGAAAGCAATTCCTGCACAT	1806
Db	24	AAATATTTCTTGAGAAATTAACCTCAATTTAAATCAAGAGAAATGCATTTCTCTGCACAT	83
QY	1807	ACAAAACCTCAGTAGAGAGAGAAACCAACCATGCTTTTGAAAAATGATTCACCCAGTGAAC	1866
Db	84	ACAAAACCTCAGTAGAGAGAGAAACCAACCATGCTTTTGAAAAATGATTCACCCAGTGAAC	143
QY	1867	TATTCGAGAAAGAACCCCTGCTTCGTAAGAAATTTGTCTCCGTTTGAGGAGATCGGAATGA	1926
Db	144	TATTCGAGAAAGAACCCCTGCTTCGTAAGAAATTTGTCTCCGTTTGAGGAGATCGGAATGA	203
QY	1927	GGAGTTGCGCATCTATTAACTTTATTTTCCACAAAATATTTTGAGAAAGCCACTCAATAG	1986
Db	204	GGAGTTGCGCATCTATTAACTTTATTTTCCACAAAATATTTTGAGAAAGCCACTCAATAG	263
QY	1987	GATTTCACTCTTGAGAAAGTAGAGCTGTGTGTCAAAATCAATATGAGAAAGCTGCTTG	2046
Db	264	GATTTCACTCTTGAGAAAGTAGAGCTGTGTGTCAAAATCAATATGAGAAAGCTGCTTG	323
QY	2047	CAATCTGAACCTGGGTTTTCCCTGCATAGAAATTTGAATTCGTGCTTTTGAAAAAAA	2106
Db	324	CAATCTGAACCTGGGTTTTCCCTGCATAGAAATTTGAATTCGTGCTTTTGAAAAAAA	383
QY	2107	TGTATTCACATACAAATCTTCACATGAGACATGTTTCATTTCCCTGTGATTAATACCT	2166
Db	384	TGTATTCACATACAAATCTTCACATGAGACATGTTTCATTTCCCTGTGATTAATACCT	443
QY	2167	AGGTAGGGGAAATGCTGGGGCCATATAGATATGACATATGTTCAAGTTCTACCAATCTTGTTTC	2226
Db	444	AGGTAGGGGAAATGCTGGGGCCATATAGATATGACATATGTTCAAGTTCTACCAATCTTGTTTC	503
QY	2227	CAGAGTAGTAGCATTTCTGTGCTCCTACCATCAACAATGAGAAATTCGGGAGCTCCAT	2286
Db	504	CAGAGTAGTAGCATTTCTGTGCTCCTACCATCAACAATGAGAAATTCGGGAGCTCCAT	563
QY	2287	GCCTTTTAAATTTTAGCCATTTCTTCTGCTMAATTTCTTAAATTAAGAGAAATTAAGTCCC	2346
Db	564	GCCTTTTAAATTTTAGCCATTTCTTCTGCTCAATTTCTT-AAATTAAGAGAAATTAAGTCCCC	622
QY	2347	GAAAGTGAACATGCTTCATGCTCACACAT	2376
Db	623	GAA-GTGGACATGCTTCATGTTACACAT	651

[illegible]

Tissue Procurement: ATCC  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: LINC674 row: b column: 05  
High quality sequence stop: 648.  
Location/Qualifiers  
1. .757

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/ano_type="vector"
/ds_xref="taxon:9606"
/clone="IMAGE:4046500"
/issue_type="from chronic myelogenous leukemia"
/lab_host="DH10B (TI phase-resistant)"
/clone_id="NH MGc 54"
/notes="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
Site_1: SfilI (ggcgcgcctggcgc); Site_2: SfilI
(ggcctatcggcgc); Double-stranded cDNA was prepared from
cell line RNA. 5' and 3' adaptors were used in cloning as
follows: 5' adaptor sequence: 5'-CACGGCCATTATGCGC-3' and
3' adaptor sequence:
5'-ATTTCAGAGCCGAGCGCGCCGACATG-dT(30)BN-3' (where B = A,
C, G or G and N = A, C, G, or T). Average insert size
1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."

```

**ORIGIN**

Query Match	19.7%	Score 562.4	DB 7	Length 757
Best Local Similarity	97.7%	Pred. No. 5e-75		
Matches 643	1	Mismatches	7	Gaps 7

QY	1886	GGTAGAAAAGCATCTTAATTGCTTTCTGTTTCAAGGTGAATTCATAAGCAACA	1745
Db	1	GGTAGAAAAGCATCTTA- TTTCGTTTTCTGTTTCAAGTGAATTCATAAGCAACA	59
QY	1746	CAATATTTCTTGAGAAATTAGCCTCATATTTAAATCAAGAGAAATGCAGTTCTCTGACA	1805
Db	60	CAATATTTCTTGAGAAATTAGCCTCATATTTAAATCAAGAGAAATGCAGTTCTCTGACA	119
QY	1806	TACAAAATCTCAGTAGAGAGAGAAACCAACCATGCTTTTGGAAAATGATTCACCCAGTGAAA	1865
Db	120	TACAAAATCTCAGTAGAGAGAGAAACCAACATGC- TTTCGAAAATGATTCACCCAGTGAAA	178
QY	1866	CTATTTCCAGAACAAACCGTCGCTCTCATATGAAATTGTCCTCGTTTGGGGATCGTGAAATG	1925
Db	179	CTATTTCCAGAACAAACCGTCCTCTCTCATATGAA- TTGTCCTCTG- TTGGGGATCGTGAAATG	236
QY	1926	AGAGATTGCCATCTATTAACTATTATTTTCCACAAAATATTTTGGAAAAGCCACTTCATA	1985
Db	237	AGAGATTGCCATCTATTAACTATTATTTTCCACAAAATA- TTTCGAAAAGCCACTTCATA	295
QY	1986	GGATTTCACCTTGGAAAAGTAGAGCTGTGTGTCAAAATCAATATATGAGAAAGCTGCCTT	2045
Db	296	GGATTTCACCTTGGAAAAGTAGAGCTGTGTGTCAAAATCAAAATATATGAGAAAGCTGCCTT	355
QY	2046	GCAATTCGAACTGGGTTTTCCCGCAATGAAATTGAAATTCGCGCTTTTGGAAAAA	2105
Db	356	GCAATTCGAACTGGGTTTTCCCGCAATGAAATTGAAATTCGCGCTTTTGGAAAAA	415
QY	2106	ATGATATTCACATACAAAATCTTCACATGAGACAGATGTTTCATTTCCCTGGATTAATACC	2165
Db	416	ATGATATTCACATACAAAATCTTCACATGAGACAGATGTTTCATTTCCCTGGATTAATACC	475
QY	2166	TAGGTAGGGGATTTCTGGGCCATATGATTAAGCATATATGTTTCAGTTCTTACCAATCT- TGT	2224
Db	476	TAGGTAGGGGATTTCTGGGCCATATGATTAAGCATATATGTTTCAGTTCTTACCAATCTGTGTT	535
QY	2225	TTCCAGAGTAGGACATTTCTGTGCTCTTACACATCAACATGTGAAGAAATTTCCGGGAGCTCC	2284

Db 536 TCACAGATAGTGCATTTCTGTGCTCTACCATACCATGTAAGAAATCCCGGAGCTCC 595  
 QY 2285 ATGCGTTTAAATTTTGGCATTTCTGT- GCGTAAATTTCTTAAATAGAAATTAAG 2341  
 Db 596 ATGGCCTTTAAATTTTGGCATTTCTGTGCTCTCATTTCTTAAATTAAGATTACAG 653

RESULT 3  
 BP183992 842 bp mRNA linear EST 31-OCT-2000  
 LOCUS 601843003F1 NIH\_MGC\_54 Homo sapiens cDNA clone IMAGE:4063848 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BP183992  
 VERSION BP183992.1 GI:11062336  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 1 (bases 1 to 842)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: sgabers-remail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LML)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LML at:  
 http://image.llnl.gov  
 Plate: L10M897 row: e column: 01  
 High quality sequence stop: 635.  
 Location/Qualifiers  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:4063848"  
 /issue\_type="from chronic myelogenous leukemia"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NIH\_MGC\_54"  
 /note="Origin: Bone marrow; Vector: pDNR-LIB (Clontech);  
 Site 1: SfiI (ggcggcctcgcc); Site 2: SfiI  
 (ggcattatcgcc); Double-stranded cDNA was prepared from  
 cell line RNA. 5' and 3' adaptors were used in cloning as  
 follows: 5' adaptor sequence: 5'-CACGGCCATTATGCGC-3' and  
 3' adaptor sequence:  
 5'-ATTCTAGAGCGCGAGCGCGCCGACATG-dt(30)BN-3' (where B = A,  
 C, or G and N = A, C, G, or T). Average insert size  
 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained  
 inserts by PCR. This library was enriched for full-length  
 clones and was constructed by Clontech Laboratories (Palo  
 Alto, CA)."

ORIGIN  
 Query Match 18.3%; Score 522.2; DB 7; Length 842;  
 Best Local Similarity 96.3%; Pred. No. 5.5e-69;  
 Matches 673; Conservative 0; Mismatches 13; Indels 13; Gaps 13;

QY 1553 GATCTCAACACTGATATTAACCCCAATTTTCCTGCTGAGGAGGACCATTC 1612  
 Db 1 GATCTCAACACTGATATTAACCCCAATTTTCCTGCTGAGGAGGACCATTC 60

QY 1613 AGCAATATATGAAATTAATCTTCTTAACCTTAAACACAGTGTATCTTGAAGTCA 1672  
 Db 61 AGCAATATATGAAATTAATCTTCTTAACTTAAACACAGTGTATCTTGAAGTCA 120

QY 1673 GGAATATATCCAGGTTACAAAGCATCTAATTTTCTTTCTGTTTCAAGTGAAT 1732

Db 121 GGAATATATCCAGGTTACAAAGCATCTTAA-TTGTCTTTCTGTTTCAAGTGAAT 179  
 QY 1733 TCACATAGCAACACATATTTCTTGGAGATTAAGCTCATATTAATCAAGAGATGC 1792  
 Db 180 TCACATAGCAACACATATTTT-TGAGAAATTAAGCTCATATTAATCAAGAGATGC 238  
 QY 1793 AGTTCTCTGACATACAAAATCTCAGTAGAGAGAAAACCAATGCTTTTGGAAATGAT 1852  
 Db 239 AGTTCTCTGACATACAAAATCTCAGTAGAGAGAAAACCAATGCTTTTGGAAATGAT 297  
 QY 1853 TCACCCAGTAAACATATTTCCAGAACAGACCTGCTCTGATGAATTTGCTCTGTTG 1912  
 Db 298 TCACCCAGTAAACATATTTCCAGAACAGACCTGCTCTGATGAATTTGCTCTGTTG 355  
 QY 1913 GGGATGATGATAGAGAGTTGGCATATTAATTAATTAATTTTCCAAAAATATTTGGAA 1972  
 Db 356 GGGATGATGATAGAGAGTTGGCATATTAATTAATTAATTTTCCAAAAATATTTGGAA 414  
 QY 1973 AGCCACTTCAATAGATTTTCACTTTGAAAAGTAGAGCTGTGTGCAAAATCAATATG 2032  
 Db 415 AGCCACTTCAATAGATTTTCACTTTGAAAAGTAGAGCTGTGTGCAAAATCAATATG 474  
 QY 2033 AGAAAGCTGCTTGCATCTGAACTTGGTTTCCCTGCAATGAAATTAATTTGCTT 2092  
 Db 475 AGAAAGCTGCC-TGCAATCTGAAC-TGGGTTTCCCTGCAATGAAATTAATTTCTG-CT 531  
 QY 2093 CTTTGTAAAAAATGATTTACATCAATCAATCTTCAATGAGACATGTTTCAATTTCCC 2152  
 Db 532 CTTTGTAAAAAATGATTTACATCAATCAATCTTCAATGAGACATGTTTCAATTTCCC 591  
 QY 2153 TTGATTAATTAATCTAGTAGAGGATTTGCGGCAATATGATTAAGATTAATTTCAAGTTCT 2212  
 Db 592 TTGATTAATTA-CTAAGTAGAGGATTTGTTGGG-CATATGATTAAGATTAAT-TCCAGTTCT 648  
 QY 2213 ACCAATCTTGTCTTCCAGATGATGACATTTCTGTCTCC 2251  
 Db 649 ACC-ATCTTGTCTTCCAGATGATGACATTTCTGTCTCAC 686

RESULT 4  
 BP282008 583 bp mRNA linear EST 16-SEP-2004  
 LOCUS BP282008 Sugano cDNA library, bone marrow K562 Homo sapiens cDNA  
 DEFINITION clone KMR03033, mRNA sequence.  
 ACCESSION BP282008.1 GI:52195740  
 VERSION BP282008  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 1 (bases 1 to 583)  
 Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,  
 Mizushima-Sugano,J., Nakai,K. and Sugano,S.  
 Sequence comparison of human and mouse genes reveals a homologous  
 block structure in the promoter regions  
 Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL PUBMED  
 15342556  
 CONTACT: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Tel: 81-3-5449-5343  
 Fax: 81-3-5449-5416  
 Email: ysuzuki@hgc.jp.  
 Location/Qualifiers  
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 /db\_xref="taxon:9606"  
 /clone="KMR03033"  
 /issue\_type="bone marrow"

ORIGIN

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/note="chronic myelogenous leukemia"

Query Match 17.6%; Score 501.8; DB 3; Length 583;

Best Local Similarity 98.6%; Pred. No. 7.3e-66; Mismatches 7; Indels 0; Gaps 0;

Matches 506; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 903 ACCAACTTGAGATGTTAAAGATTTGACACCAATTTTACATATGTCACAGTCAGAT 962  
Db 71 AGCAGATGAGACTGTTAAAGATTTGACACCAATTTTACATATGTCACAGTCAGAT 130  
QY 963 TCTACTGAGCCAAACATTAGTATGTTTCAAGTAGATGTCAGAAACAGGAAAA 1022  
Db 131 TCTACTGAGCCAAACATTAGTATGTTTCAAGTAGATGTCAGAAACAGGAAAA 190  
QY 1023 GGTACTGGCAGCCTTGAGATTCACCGTTTTTTCATAAACCTGAAACAGTTCCCAAG 1082  
Db 191 GGTACTGGCAGCCTTGAGATTCACCGTTTTTTCATAAACCTGAAACAGTTCCCAAG 250  
QY 1083 TCACATCAAAAGAGATTCACATGACATGAAATTCGGGCTTACAGTTGCTTCATCT 1142  
Db 251 TCACATCAAAAGAGATTCACATGACATGAAATTCGGGCTTACAGTTGCTTCATCT 310  
QY 1143 CTACAGGGCAGCCTTACTTCTGACACAGAGAGACATGACCTTTTATGGGAATGATG 1202  
Db 311 CTACAGGGCAGCCTTACTTCTGACACAGAGAGACATGACCTTTTATGGGAATGATG 370  
QY 1203 TCTTTGCTGTATGTTGTCAATCTTTCTTTGATTTGGATTTTAAACATCTCCGAA 1262  
Db 371 TCTTTGCTGTATGTTGTCAATCTTTCTTTGATTTGGATTTTAAACATCTCCGAA 430  
QY 1263 CTGGGATTTAAAGAGATCTTATGTTTATACCAAGGCTTTTAAAGATTTCTTA 1322  
Db 431 CTGGGATTTAAAGAGATCTTATGTTTATACCAAGGCTTTTAAAGATTTCTTA 490  
QY 1323 ATATGAAAAACAGCAATGTTGTAATAATGCTACAGAAATAGTGAATTATATTA 1382  
Db 491 ATATGAAAAACAGCAATGTTGTAATAATGCTACAGAAATAGTGAATTATATTA 550  
QY 1383 ATTCCAGTGAAGCAGTCTTATATGTTGATCCCA 1415  
Db 551 ATTCCAGTGAAGCAGTCTTATATGTTGATCCCA 583

RESULT 5  
CD708943 602 bp mRNA linear EST 25-JUN-2003  
LOCUS CD708943  
DEFINITION EST25470 human nasopharynx Homo sapiens cDNA, mRNA sequence.  
ACCESSION CD708943  
VERSION CD708943.1 GI:32239573  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 602)  
AUTHORS Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.  
JOURNAL Transcriptional Gene Expression Profile of Human Nasopharynx  
COMMENT Unpublished (2003)  
Contact: Yixin Zeng  
Cancer Center  
Sun Yat-sen University  
651 Dongfeng Road East, Guangzhou 510060, China  
Tel: 86-1380-9770-743  
Fax: 86-20-8775-4506  
Email: yxzeng@zsuns.edu.cn.  
Location/Qualifiers  
1. .602  
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ORIGIN

/mol\_type="mRNA"  
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/clone\_lib="human nasopharynx"  
/note="RSTS generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN

Query Match 17.5%; Score 499.6; DB 5; Length 602;

Best Local Similarity 99.8%; Pred. No. 1.6e-65; Mismatches 0; Indels 0; Gaps 0;

Matches 499; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 28 CAGCCAAAGAGGTGGACGCTGGCTCTGAGATGGAATATGCTTCAACAGGTTGA 87  
Db 103 CAGCCAAAGAGGTGGACGCTGGCTCTGAGATGGAATATGCTTCAACAGGTTGA 162  
QY 88 AGAGGGAACAGCTTTTCTGCTTCACACATGAAATGACATGCTTCAATGGGATG 147  
Db 163 AGAGGGAACAGCTTTTCTGCTTCACACATGAAATGACATGCTTCAATGGGATG 222  
QY 148 AGTATAGCCCTTACATCTCTTCACTGCTGCTGCTGATGATGAGAAATTACAAATATAA 207  
Db 223 AGTATAGCCCTTACATCTCTTCACTGCTGCTGCTGATGATGAGAAATTACAAATATAA 282  
QY 208 CTCTGGCCACATCTGGGTGAAACAGCCCAATTTTAAAGATGGATATATCTCTAT 267  
Db 283 CTCTGGCCACATCTGGGTGAAACAGCCCAATTTTAAAGATGGATATATCTCTAT 342  
QY 268 ATATGGCCAAAGAGCAATTTAAGATGCTGCAACCAAGAACTTCAATTTTATATAAATGG 327  
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Db 403 CATCAAGAAAGATTTCAATCAACAAAGATTAATAAACAACAGCTGGCTTTGTATTA 462  
QY 388 AATCTTCTGGAACCAATGCTTCTATGATGCACTGCTGATGCTCCAAACATTTTCA 447  
Db 463 AATCTTCTGGAACCAATGCTTCTATGATGCACTGCTGATGCTCCAAACATTTTCA 522  
QY 448 AGAGCACTGATATGAGAAAGACATTTCTTCTGATATCCGCGAGATATTCCTGATGA 507  
Db 523 AGAGCACTGATATGAGAAAGACATTTCTTCTGATATCCGCGAGATATTCCTGATGA 582  
QY 508 AGTAACTGTGCTATTATG 527  
Db 583 AGTAACTGTGCTATTATG 602

RESULT 6  
AG154727 628 bp DNA linear GSS 09-JAN-2002  
LOCUS AG154727  
DEFINITION Pan troglodytes DNA, clone: RP43-018N08.T7, genomic survey  
sequence.  
ACCESSION AG154727  
VERSION AG154727.1 GI:16684405  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes

REFERENCE 1  
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
Totoki,Y., Watanabe,H. and Sakaki,Y.  
JOURNAL BAC end sequences of Library RRC1-43  
COMMENT Unpublished  
2 (bases 1 to 628)  
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
Totoki,Y., Watanabe,H. and Sakaki,Y.  
JOURNAL Direct Submission  
Submitted (02-AUG-2001) Aseo Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

FEATURES  
Source 1. .602  
/organism="Homo sapiens"



1-7-22 Shehito-chou, Tsuiri-mi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail: [chimbpeesgc.riken.go.jp](mailto:chimbpeesgc.riken.go.jp), URL: <http://bgp.gsc.riken.go.jp/>,  
Tel:81-45-503-9111 Fax:81-45-503-9170)  
Clones are derived from the chimpanzee BAC library RRC1-43 This BAC  
end was generated during the Kd process and may have higher chance  
of clone tracking errors.  
PRIMERS

**ORIGIN**

Query Match	17.5%;	Score 499.6;	DB 14;	length 628;
Best Local Similarity	94.3%;	Pred. No. 1.5e-65;		
Matches 561; Conservative	1;	Mismatches 26;	Indels 7;	Gaps 4;

Qy	1743	CGACAAATTTCTTGGAAATTAAGCCCTCATTTAAATCAAGAGAAATGCAAGTCTCCG	1802
Db	23	ACACATATTTCTTGAGAAATTTAACCCCTCATTTTAATCAAGAGAAATGCAAGTCTCCG	82
Qy	1803	ACATACAAAACCTCAGTAGAGAGGAAACCAACCATCTTTTGGAAAATGATTCACCAGTG	1862
Db	83	ACATACAAAACCTCAGTAGAGAGGAAACCAACCATCTTTTGGAAAATGATTCACCAGTG	142
Qy	1863	AAACTATTTCCAGAACAGACCCTGCTTCTGATGAATTTGTCTCCTGTTTGGGAGATCGGA	1922
Db	143	AAACTATTTCCAGAACAGACCCTGCTTCTGATGAATTTGTCTCCTGTTTGGGAAATCGGA	202
Qy	1923	ATGAGAGATTGCATCTATTAATACTTAATTTTCCAAAAATATTTTGGAAAGCACTTCA	1982
Db	203	ATGAGAGATTGCATCTATTAATACTTAATTTTCCAAAAATATTTTGGAAAGCACTTCA	262
Qy	1983	ATGAGATTTCACTCTTGGAAAAAGTAGAGCTGTGTGTCATAATCATATGAGAAAGCTGC	2042
Db	263	ATGAGATTTCACTCTTGGAAAAAGTAGAGCTGTGTGTCATAATCATATGAGAAAGCTGC	322
Qy	2043	CTTGCAATCTGAACCTGGGTTTTCCCTGCAATAGAAATTTGAATTCGCTCTTTTGAAA	2102
Db	323	CTTGCAATCTGAACCTGGGTTTTCCCTGCAATAGAAATTTGAATTCGCTCTTTTGAAA	382
Qy	2103	AAATATTTTCAACATACAAATCTTCAACATGACAAATGTTTTCAATTCCTCTGGATAAT	2162
Db	383	AAATATTTTCAACATACAAATCTTCAACATGACAAATGTTTTCAATTCCTCTGGATAAT	442
Qy	2163	ACCTAGTAGAGGAGATTTGCTGGGCCATATGATATGATATGTTTCACTTCAACAA--TCT	2220
Db	443	ACCTAGTAGAGGAGATTTGCTGGGCCATATGATATGATATGTTTCACTTCAACATCTCT	502
Qy	2221	TGTTTCCAGAGTAGTGACA-TTCTGTGCTCCTACATCACCAGTAA-GAATTCGCGGG	2278
Db	503	GGTTTCCAGAGTAGTGACATTTTGTGCTCCTACATCACCAGTAAATTCGCGGG	562
Qy	2279	AGCTCCATGCTTTTTAA---TTTTAGCATCTTCACGCTAATTTCTTAAATTT	2330
Db	563	AGCTCCATGCTTTTTAAATTTTAAAGCATTTCTTGCCTATTTCTTAAATTT	617

RESULT	7
LOCUS	BF210400
DEFINITION	BF210400 754 bp mRNA linear EST_06-NOV-2000 601874484r1 NIH_MGC_54 Homo sapiens CDNA clone IMAGE:4101164 5', mRNA sequence.

ACCESSION	BF210400
VERSION	BF210400.1
KEYWORDS	EST.
SOURCE	Homo sapiens (human)

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (pages 1 to 754)	NIH-MGC	<a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .	National Institutes of Health, Mammalian Gene Collection (MGC).	Unpublished (1999)
	Contact: Robert Strauberg, Ph.D.			

CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
plate: LLCM872 row: g column: 21  
High quality sequence stop: 650.

## FEATURES

**Source**

Query Match	17.1%	Score 488.4	DB 7	Length 754
Best Local Similarity	93.7%	Pred. No. 7.1e-64		
Matches 564	Conservative 0	Mismatches 31	Indels 7	Gaps 5

OY	903	ACCAAACTTGGAAATGTTAAAGAAATTGACACCAATTTTACATATGTGCACACGTCCAGAT	962
Db	71	AGCCATGTGGAACTGTTAAAGAAATTGACACCAATTTTACATATGTGCACACGTCCAGAT	130
OY	963	TCCTACTTGGAGCCGAAACATTAAATACGTAATTTCAAGTGAATGTCAAGAAACAGCCAAA	1022
Db	131	TCCTACTTGGAGCCGAAACATTAAATACGTAATTTCAAGTGAATGTCAAGAAACAGCCAAA	190
OY	1023	GGTACTGGCAGCCCTTGGAGTTCACCGGTTTTTTCATTAACACCTGAAACAGTCCCCAGG	1082
Db	191	GGTACTGGCAGCCCTTGGAGTTCACCGGTTTTTTCATTAACACCTGAAACAGTCCCCAGG	250
OY	1083	TCACATCAAAAGCATTTCAACATGACACATGGAAATTCGGGCTAACAGTTCCTCCACT	1144
Db	251	TCACATCAAAAGCATTTCAACATGACACATGGAAATTCGGGCTAACAGTTCCTCCACT	310
OY	1143	CTACAGGCGACCTTACTTCTGACAAACAGAGAGACATTGCACTTTATTTGGAAATGATCG	1202
Db	311	CTACAGGCGACCTTACTTCTGACAAACAGAGAGACATTGCACTTTATTTGGAAATGATCG	370
OY	1203	TCCTTGCCTGTATGTTGTCAATTCCTTTCTTTGATTTGGAAATTTTAAAGATCATTTCCGA	1264
Db*	371	TCCTTGCCTGTATGTTGTCAATTCCTTTCTTTGATTTGGAAATTTTAAAGATCATTTCCGA	430

QY 1263 CTGGATTAAAGAGATCTTATTTGTTATACCAAGTGGCTTTATGAGATATTCCTA 1322  
 DB 431 -TGGATTAAAGAGATCTTATTTGTTATACCAAGTGG-TTTATGAGATATTCCTA 488  
 QY 1323 AATGAAAAACGCAATGTTTGAAAAATGCTACAGAAAAATAGTGAATTAATAA 1382  
 DB 489 AATGAAAAACGCAATGTTTGAAAAATGCTACAGAAAAATAGTGAATTAATAA 548  
 QY 1383 ATTCGATGAGCAGCTCTATATGTTGATCCCATGATTAACAGATTAAGAAATCTCA 1442  
 DB 549 ATTCGATGAGCAGCTCTATATGTTGATCCCATGATTAACAGATTAAGAAATCTCA 607  
 QY 1443 TCCAGAACACAGCCTACAGACTACAGAGAGAAATACAGAGCCCTGGAGACAAG 1502  
 DB 608 TCC---AGAACAAAGCTACAGACTACAGAGAG-GAATACAGAGCCCTGGAGACAAG 663  
 QY 1503 AC 1504  
 DB 664 AC 665

RESULT 8  
 BF238439 917 bp mRNA linear EST 14-NOV-2000  
 LOCUS 601904735F1 NIH\_MGC\_54 Homo sapiens cDNA clone IMAGE:4132593 5',  
 DEFINITION mRNA sequence.

ACCESSION BF238439  
 VERSION BF238439.1 GI:11152359  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 1 (bases 1 to 917)  
 NIH-MGC http://mgs.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: CLONTECH Laboratories, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINL at:  
 http://image.jnl.gov  
 Plate: LLCM1032 row: e column: 10  
 High quality sequence steps: 575.  
 Location/Qualifiers

FEATURES  
 source

1.917  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4132593"  
 /tissue\_type="from chronic myelogenous leukemia"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NIH\_MGC\_54"  
 /note="Organ: Bone marrow; Vector: pDNR-LIB (Clontech);  
 Site 1: SfiI (ggcgctcgccg); Site 2: SfiI  
 (ggccatctggcc); Double-stranded cDNA was prepared from  
 cell line RNA. 5' and 3' adaptors were used in cloning as  
 follows: 5' adaptor sequence: 5'-CACGGCATTAATGCGC-3' and  
 3' adaptor sequence: 5'-ATCTAGAGCGCGAGCGGCGACATG-dt(30)BN-3' (where B = A,  
 C, or G and N = A, C, G, or T). Average insert size  
 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained  
 inserts by PCR. This library was enriched for full-length  
 clones and was constructed by Clontech Laboratories (Palo  
 Alto, CA)."

Query Match 16.9%; Score 482.6; DB 7; Length 917;  
 Best Local Similarity 90.5%; Pred. No. 5e-63;  
 Matches 583; Conservative 0; Mismatches 50; Indels 11; Gaps 6;

QY 903 ACCAACTTGGAAATGTTAAAGAAATTTGACACCAATTTTCAATATGCAACAGTCGAAT 962  
 DB 71 AGCAGTGAACCTGTTAAAGAAATTTGACACCAATTTTCAATATGCAACAGTCGAAT 130  
 QY 963 TCTACTTGAGCCCAACATTAAGTACGATTTTCAAGTGAATGTCAAGAAACAGGCAAAA 1022  
 DB 131 TCTACTTGAGCCCAACATTAAGTACGATTTTCAAGTGAATGTCAAGAAACAGGCAAAA 190  
 QY 1023 GGTACTGAGCAGCTTGGAGTTCAACGTTTTTTCATTAACACCTGAACAGTTCCCAAG 1082  
 DB 191 GGTACTGAGCAGCTTGGAGTTCAACGTTTTTTCATTAACACCTGAACAGTTCCCAAG 250  
 QY 1083 TCACATCAAAAGATTCACAACTGACACATGGAATCT--GGGCTAACAGTGGCTTCATC 1141  
 DB 251 TCACATCAAAAGATTCACAACTGACACATGGAATCTGGGCTAACAGTGGCTTCATC 310  
 QY 1142 TCTACAGGACCTTACTTCTGACACACAGAGAGACATTGACCTTTATTTGGGAATGATC 1201  
 DB 311 TCTACAGGACCTTACTTCTGACACACAGAGAGACATTGACCTTTATTTGGGAATGATC 370  
 QY 1202 GTCTTGTCTGTATATGTTGCAATCTTCTTTGATTTGGGATATTTAAACAGATTCCTGA 1261  
 DB 371 GTCTTGTCTGTATATGTTGCAATCTTCTTTGATTTGGGATATTTAAACAGATTCCTGA 430  
 QY 1262 ACTGGATTAAAGAAAGATCTTATGTTAATACCAAGTGGCTTATGAAATATTCCT 1321  
 DB 431 ACTGGATTAAAGAAAGATCTTATGTTAATACCAAGTGGCTTATGAAATATTCCT 488  
 QY 1322 AATATGAAAAACGCAATGTTTGAAAAATGCTACAGAAAAATAGTGAATTAATAA 1381  
 DB 489 AATATGAAAAACGCAATGTTTGAAAAATGCTACAGAAAAATAGTGAATTAATAA 548  
 QY 1382 AATTCAG-TAGACAGTCTTATATGTTATGATCCATGATTAACAGATTAAGAAATCTT 1440  
 DB 549 AATTCAGTGTGACAGTCTTATATGTTATGATCCATGATTAACAGATTAAGAAATCTT 608  
 QY 1441 CATCCAGAACCAAGCCTACAGACTACAGAGAGAAATACAGAGCCCTGGAGACAAG 1500  
 DB 609 CATCCAGAACCAAGCCTACAGACTACAGAGAGAAATACAGAGCCCTGGAGACAAG 665  
 QY 1501 AGACTACCCGCAAAACTCGCTATTGCAACAATCTACAGTGTGAT 1544  
 DB 666 AGATAAC-----GAATCGCTATTGCAAAATCTACAGTGTGAT 705

RESULT 9  
 BF209716 820 bp mRNA linear EST 06-NOV-2000  
 LOCUS 601874259F1 NIH\_MGC\_54 Homo sapiens cDNA clone IMAGE:4098831 5',  
 DEFINITION mRNA sequence.

ACCESSION BF209716  
 VERSION BF209716.1 GI:11103302  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 1 (bases 1 to 820)  
 NIH-MGC http://mgs.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: CLONTECH Laboratories, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be

ORIGIN





DEFINITION	AGENCOURT 7594668 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6061504					
ACCESSION	5', mRNA sequence.					
VERSION	BQ228535					
KEYWORDS	BQ228535.1 GI:20409935					
SOURCE	EST.					
ORGANISM	Homo sapiens (human)					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.					
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.					
TITLE	1 (bases 1 to 916)					
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)					
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cs9pbs-remail.nih.gov Tissue Procurement: ATCC/DCTD/BTP cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: LLM1333 Row: h Column: 17 High quality sequence stop: 554.					
FEATURES	Location/Qualifiers					
source	1..916 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6061504" /tissue_type="melanotic melanoma" /lab_host="DH10B (phage-resistant)" /note="Organ: skin; Vector: pCMV-SPORT6; Site:1: NciI; Site:2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2 kb. Library constructed by Life Technologies."					
ORIGIN						
Query Match	14.9%; Score 424.8; DB 3; Length 916;					
Best Local Similarity	93.1%; Pred. No. 2.6e-54;					
Matches 512; Conservative	0; Mismatches 27; Indels 11; Gaps 6;					
OY	1258	CGGAATGGGATTAAAGAAGAGATTTATGTATATACCAAGTGCGTTTAGAAGATAT	1311	TT		
Db	221	CTGAAACGSGATTAAAGAGAGATCTTATGTATATACCAAGTGCGTTTAGAAGATAT	280			
OY	1318	TCTTAATATGAAAAACAGCAATGTTGTGAAAATGCTACAGAAAAATAGTGAAC TTATGA	1377			
Db	281	TCTTAATATGAAAAACAGCATGTGTGAAAATGCTACAGAAAAATAGTGAAC TTATGA	340			
OY	1378	TAAATATTCACGTAGACAGTGCTCTATATGTTGATCCCATGATTCACAGATPAAAATAAT	1437			
Db	341	TAAATATTCACGTAGACAGTGCTCTATATGTTGATCCCATGATTCACAGATPAAAATAAT	400			
OY	1438	CTTCATGCCGAACAACAAGCCTACAGATTAACAAGAGAAATACAGACCCTCGGAAC	1497			
Db	401	CTTCATGCCGAACAACAAGCCTACAGATTAACAAGAGAAATACAGACCCTCGGAAC	460			
OY	1498	AAGAGACTACCCGCAAACCTCGTATTGACAACTACTACAGTGTATATTTCTCGTACT	1557			
Db	461	AAGAGACTACCCGCAAACCTCGTATTGACAACTACTACAGTGTATATTTCTCGTACT	520			
OY	1558	CAACACTGATATTAACCCCAAATTTCCAATTTTTCTGCTGAGGAGAACCTTCAGCA	1617			
Db	521	CAACACTGATATTAACCCCAAATTTCCAATTTTTCTGCTGAGGAGAACCTTCAGCA	580			
OY	1618	TAAATATGAATTTCTTCTTAACTTAACCTTAACCA - GTGATTCCTTAAGCTCAGGA	1676			
Db	581	TAAATATGAATTTCTTCTTAACTTAACCTTAACCA - GTGATTCCTTAAGCTCAGGA	640			
OY	1677	ATAATCCCA - GTTACAAAGACATCTTAATTTTGCTTTTCT -- GTTCAAGTGTGAT	1732			

Db	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	Source
Db	641	ATATATCCAGGGTTACAAAAGCATCTTAATTTTGCTTTTCGTGTTCCAGGGGGAAT	1733	T--CACTAAGCACACAAATATTCTT--GGAGAAATTAGCCTCAT--ATTAAATCAAGCA	1786								
Db	701	TTCCCTAAGCCAAACCCATATTTCTTTGGAGAAATTAAAGCCTCCTTATTAATCAGGAGA	760										
Qy	1787	GAATGACGATT 1796											
Db	761	GAATGACGATT 770											
RESULT 13													
BP239183													
LOCUS	BP239183	513 bp	mrna	linear	EST 14-NOV-2000								
DEFINITION	60190558.F1 NIH_MGC_54	Homo sapiens	CDNA clone	IMAGE:4133421	5'								
ACCESSION	BP239183												
VERSION	BP239183.1	GI:11153104											
KEYWORDS	EST												
ORGANISM	Homo sapiens (human)												
SOURCE	Homo sapiens												
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;												
AUTHORS	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;												
TITLE	Hominidae; Homo.												
JOURNAL	1 (bases 1 to 513)												
COMMENT	NIH-MGC http://mgc.nci.nih.gov/												
	National Institutes of Health, Mammalian Gene Collection (MGC)												
	Unpublished (1999)												
	Contact: Robert Straube, Ph.D.												
	Email: gspds-remail.nih.gov												
	Tissue Procurement: ATCC												
	CDNA Library Preparation: CLONTECH Laboratories, Inc.												
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)												
	DNA Sequencing by: Incyte Genomics, Inc.												
	Clone distribution: MGC clone distribution information can be												
	found through the I.M.A.G.E. Consortium/LNLN at:												
	http://image.lnl.gov												
	Plate: LCM1034 row: 9 column: 22												
	High quality sequence stop: 502.												
	Location/Qualifiers												
	1..513												
	/organism="Homo sapiens"												
	/mol_type="mRNA"												
	/db_xref="taxon:9606"												
	/clone="IMAGE:4133421"												
	/tissue_type="from chronic myelogenous leukemia"												
	/lab_host="DH10B (T1 phage-resistant)"												
	/clone_id="NIH_MGC_54"												
	/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);												
	Site 1: SfiI (ggcgctcgccg); Double-stranded cDNA was prepared from												
	cell line RNA. 5' and 3' adaptors were used in cloning and												
	follows: 5' adaptor sequence: 5'-CACGGCCATTATGCGC-3' and												
	3' adaptor sequence:												
	5'-ATTCTAGGCGCGAGCGCGCGCATG-dt(30)BN-3' (where B = A,												
	C, or G and N = A, C, G, or T). Average insert size												
	1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained												
	inserts by PCR. This library was enriched for full-length												
	clones and was constructed by Clontech Laboratories (Palo												
	Alto, CA)."												
ORIGIN													
Query Match	12.4%	Score 3											

Db 133 TCTACTTGAGCCAAACATTAAAGTACGTAATTTCAAGTAGAGATGTCCAGAAACAGGCACA 192  
 QY 1021 AAGGTACTGGCAGCCTTGG-AGTTCACCGTT-TTTCATATAACACCTGAAACAGTTCCTC 1078  
 Db 193 AAGGTACTGGCAGCCTTGGAAAGTTACCGTGTTCATATAAACACCTGAAACAGTTCCTC 252  
 QY 1079 CAGGTACATCAAAAGACATTCGAA-CAATGACATGGAATTTGGGCTTAACAGTTCCTC 1137  
 Db 253 CAGGTACATCAAAAGACATTCGAAAGATGACATGGAATTTGGGCTTAACAGTTCCTC 312  
 QY 1138 CATCTTACAGGGCAGCTTACTTCTGACAAAGAGAGAC-ATTGACCTTTTATATGGA 1195  
 Db 313 CATCTTACAGGGCAGCTTACTTCTGACAAAGAGAGACATTTGGAATTTATGGA 372  
 QY 1196 ATGATGCTCTTGTCTGTATGTGTCATCTTCTTGTGATGGAGATTTTACAGATCA 1255  
 Db 373 ATGATGCTCTTGTCTGTATGTGTCATCTTCTTGTGATGGAGATTTTACAGATCA 432  
 QY 1256 TTCCGAAGCTGGAGTTAAAGAGAGATCTTAATGTAAATACAAAGTGGCTTTATGGAAT 1315  
 Db 433 TTCCGAAGCTGGAGTTAAAGAGAGATCTTAATGTAAATACAAAGTGGCTTTATGGAAT 492  
 QY 1316 ATTCTTAATTTGAAAAACAGC 1336  
 Db 493 ATTCTTAATTTGAAAAAGAGC 513

RESULT 14  
 LOCUS CB429984 720 bp mRNA linear EST 25-MAR-2003  
 DEFINITION 605838 MARC 6BOV Bos taurus cDNA 3', mRNA sequence.  
 ACCESSION CB429984  
 VERSION CB429984.1 GI:29205578  
 KEYWORDS EST.  
 SOURCE Bos taurus (cattle)  
 ORGANISM Bos taurus  
 Buiakytoca; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 Pecora; Bovidae; Bovinae; Bos.  
 1 (bases 1 to 720)  
 Smith,T.P.L., Roberte,A.J., Echtenkamp,S.E., Chitko-McKown,C.G.,  
 Wray,J.E. and Keele,J.W.  
 A second set of bovine ESTs from pooled-tissue normalized libraries  
 Unpublished (2003)  
 Contact: Smith TPL  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366  
 Fax: 402 762 4390  
 Email: smith@email.marc.usda.gov  
 Single pass sequencing. Bases called with phred v0.020425.c and  
 trimmed with the aid of the trim\_alt option. Vector identified with  
 cross\_match v0.990329.  
 Plate: FQY8023 row: G column: 9  
 Seq primer: TAGAAGGACAGTCGAGG.  
 Location/Qualifiers  
 1..720  
 /organism="Bos taurus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9913"  
 /issue\_type="pooled"  
 /lab\_host="DH10B"  
 /clone\_lib="MARC 6BOV"  
 /note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;  
 library made with RNA pooled from multiple tissues  
 including liver, lung, hypothalamus, pituitary, and  
 placenta/endometrium."

## ORIGIN

Query Match 12.1%; Score 345.6; DB 4; Length 720;  
 Best Local Similarity 82.9%; Pred. No. 2.5e-42;  
 Matches 393; Conservative 1; Mismatches 80; Indels 0; Gaps 0;

QY 473 ATTTCTTGAGATATCCGACGATATTTCTGATGAAGTAACTGTGTCTATTTATGATAT 532  
 Db 626 ATTTTAAAGATGATATCCAGATGTATCTTGACAAAGTACCGTGTATTTATGATAT 567  
 QY 533 TCAGGACATGATCTTGACCTGGAATGCTGGAAGCTACCTACATATGACACAAATATAC 592  
 Db 566 TCTGGCAACATGATCTTGACCTGGAACATGGAAGCCCACTTACATAGACAAAGTAT 597  
 QY 593 GTGTGATCATGTGAGAGTTTGAAGACAGAAAGACCAACATATCTCACTCAAGCTAT 652  
 Db 506 GTGTGTAGTGAAGAGTTTGAAGACAGAAAGACCAAGAAATATCTCACTCAAGTAC 447  
 QY 653 ATTAACATCTCCACTGATTTATTCAGAGGTGCGAAGATGATCTGTGGTCCAGCA 712  
 Db 446 ATTAACATCTCCACTGATTTATTCAGAGGTGCGAAGATGATCTGTGGTCCAGCT 387  
 QY 713 GCAAGCACTAGGACATGGAAGATGCAAAACATGCAATTCACCTGATGATATAGTG 772  
 Db 386 TCMAATGTTCTGGGACATGGAAGATGCAAAACATGCAATTCATCTGACATATAGTG 327  
 QY 773 ATACCTTTCAGAGCCGTCATTTCCAGGCTGAGACTATTAATGCTACAGTGCCCAAGCC 832  
 Db 326 ATACCTTTCAGATTCATTTTCCAGGCTGAGATATTAATGCTACAGTGCCCAAGCT 267  
 QY 833 ATTAATTTATGGGATAGTCAACACATTTGAAAGGTTTCTGTGAAATGATATCAAG 892  
 Db 266 GTAATCCACTGGGATAGTCAACACATTTGAAAGGTTTCTGTGAAATGATATCAAA 207  
 QY 893 GCTACACAAACCAACTTGAATGTTAAAGATTTGACCAATTTTACATAT 946  
 Db 206 GATACACAAACCAACTTGAACGTAACTAATTTACTTCTTTCATATGT 153

RESULT 15  
 LOCUS BF212748 540 bp mRNA linear EST 06-NOV-2000  
 DEFINITION 60181391F1 NIH\_MGC\_54 Homo sapiens cDNA clone IMAGE:4048150 5',  
 mRNA sequence.  
 ACCESSION BF212748  
 VERSION BF212748.1 GI:11106334  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Buiakytoca; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini;  
 Homidae; Homo.  
 1 (bases 1 to 540)  
 NIH-MGC http://mgs.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-r@mail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: LNC878 row: F column: 23  
 High quality sequence stop: 540.  
 Location/Qualifiers  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:4048150"  
 /issue\_type="from chronic myelogenous leukemia"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NIH MGC 54"  
 /note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);  
 Site 1: SfiI (ggcgctcgagc); Site 2: SfiI  
 (ggcattatggcc); Double-stranded cDNA was prepared from

## FEATURES

## source





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PT /note="If the base at this position is G (encoding Gly),  
PT the base at position 127 is also G (encoding Gln). If the  
PT base at this position is A (encoding Arg) the base at  
PT position 127 is T (encoding His)"  
XX  
XX MO200185790-A2.  
XX  
XX 15-NOV-2001.  
XX  
XX 10-MAY-2001, 2001MO-US015057.  
XX  
XX 10-MAY-2000, 2000US-0203426P.  
XX  
XX (SCHE ) SCHERING CORP.  
XX  
XX Chirica M, Kaetelein RA, Moore KM, Parham CL;  
XX  
XX MPI, 2002-062238/08.  
XX P-PSDB; AAO14008.  
XX  
XX Novel DNAX cytokine receptor subunit 5 polypeptide which is subunit of  
PT receptor complex for p40/IL-830, useful for treating conditions  
PT associated with abnormal expression or triggering of response to p40/IL-  
PT 830 ligand.  
XX  
XX Claim 18; Page 9-12; 74bp; English.  
XX  
XX The present cDNA sequence encodes the human DNAX cytokine receptor  
CC subunit 5 (defined as DCRS5 or IL30 receptor) of the invention. DCRS5 is  
CC a member of the class I branch of the cytokine receptor superfamily and  
CC is closely related to the IL-6 receptor subunit gp130 and the IL-12R-Beta  
CC -2 subunit. Cytokines are soluble molecules which play a critical role in  
CC controlling the complex cellular interactions of the immune response. The  
CC invention comprises novel receptors related to cytokine receptors  
CC designated DNAX cytokine receptor subunits (DCRS). Specifically the  
CC invention comprises a subunit (DCRS5) for a receptor complex for the  
CC p40/IL-830 ligand. The DCRS5 proteins of the invention are useful for  
CC treating diseases or disorders associated with abnormal expression or  
CC abnormal triggering of response to the p40/IL-830 ligand. The proteins of  
CC the invention can be used to modulate the physiology or development of a  
CC cell from a host which exhibits TH1-mediated disease; multiple sclerosis;  
CC rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
CC diabetes; psoriasis; sepsis; an allogeneic transplant recipient; chronic  
CC TH2 response; tumour; viral or fungal growth; vaccine recipient; or an  
CC allergic response  
XX  
XX Sequence 2859 BP; 929 A; 575 C; 560 G; 791 T; 0 U; 4 Other;  
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Query Match 100.0%; Score 2857.4; DB 6; Length 2859;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2859; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 61 GGAATTATGCTCTTCAACAGGTTGAAAGAGGGAACAGCTTTTCTGCTTCAAGCAT 120  
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DB 181 TCATGAGAGATTCACAAATTAACCTGCTGCGCACATCTGGGTAGAACACGACCAAT 240  
QY 241 TTTTAAAGATGGGTATGATATCTCTATATATGCGCAAGACAAATTAAGAACTGCCAAC 300  
DB 241 TTTTAAAGATGGGTATGATATCTCTATATATGCGCAAGACAAATTAAGAACTGCCAAC 300  
QY 301 AAGGAACTTCATTTTATTAATAAATGCGATCAAGAAAGATTTCAATCAAGAAATTA 360

DB |||||  
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QY |||||  
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QY |||||  
DB 361 TAAACACAGCTCGGCTTTGGATTAATAAATTTCTGGAACCAATGCTTCTATGACTG 420  
QY |||||  
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DB 481 TGGATATCGGCGACGATATTCCTGATGAAGTAACCTGTGCTATTAAGATTTCAAGGCA 540  
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DB 601 TGTGAAGATTTAGACAGAGAGAGAGACAGATCTCACTCAAGCTATATTAACAT 660  
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 Db 2821 GCACCAAGACCAAACTCTGTCTGGAATAAAAAAAAAAAAAA 2859

RESULT 2  
 ADS73604  
 ID ADS73604 standard, cDNA, 2859 BP.  
 XX  
 AC ADS73604;  
 XX  
 DT 16-DEC-2004 (first entry)  
 XX  
 DE Human IL-23r coding sequence.  
 XX  
 KW se; gene; human; interleukin 23; subunit p19; IL-23; IL-23p19; tumour;  
 KW growth; agonist; antagonist; receptor; cancer; antigen-binding site;  
 KW antibody; extracellular region; antisense nucleic acid;  
 KW small interference RNA; siRNA; polyclonal; monoclonal; humanized; Fab;  
 KW Fv; F(ab')2; peptide mimetic; colon; ovarian; breast; melanoma; cachexia;  
 KW anorexia; angiogenesis; gastrointestinal tract; respiratory tract;  
 KW reproductive system; endocrine system.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 119..2008  
 FT /tag= b  
 FT /product= "IL-23r"  
 FT sig\_peptide 119..187  
 FT /tag= a  
 FT mat\_peptide 188..2005  
 FT /tag= c  
 XX  
 PN MO2004081190-A2.  
 XX  
 PD 23-SEP-2004.  
 XX  
 PF 09-MAR-2004; 2004MO-US007198.  
 XX  
 PR 10-MAR-2003; 2003US-0453672P.  
 XX  
 PA (SCHE) SCHERRING CORP.  
 XX  
 PI Ofc M, Mcclanahan TK;  
 XX  
 DR WPI: 2004-668951/65.  
 DR P-PSDB; ADS73605.  
 XX  
 PT Modulating tumor growth, useful for treating a subject suffering from  
 cancer or tumor, comprises contacting a tumor cell with an agonist or  
 antagonist of IL-23.

XX Claim 4; SEQ ID NO 5; 57bp; English.  
 PS This sequence encodes human interleukin 23 receptor (IL-23R). The method  
 XX of the invention for modulating tumour growth comprises contacting a  
 CC tumour cell with an agonist or antagonist of IL-23. The agonist or  
 CC antagonist is a binding composition which specifically binds the IL-23  
 CC p19 subunit (IL-23p19) or the IL-23R protein. The identified agonist or  
 CC antagonist may be used for diagnosing or treating a subject suffering  
 CC from a cancer or tumour. The binding composition comprises an antigen-  
 CC binding site of the antibody, an extracellular region of IL-23R, a small  
 CC molecule, an antisense nucleic acid or small interference RNA (siRNA), or  
 CC a detectable label. The binding composition comprises a polyclonal  
 CC antibody, a monoclonal antibody, a humanized antibody or its fragment, a  
 CC Fab, Fv, F(ab')<sub>2</sub> fragment, or a peptide mimetic of an antibody. The  
 CC tumour cell is a colon, ovarian or breast cancer cell, or melanoma cell.  
 CC In the treatment method, the antagonist of IL-23 inhibits growth of  
 CC cancer or tumour, cachexia, anorexia or angiogenesis. The cancer or  
 CC tumour is of the gastrointestinal tract, respiratory tract, reproductive  
 CC system or endocrine system. In diagnosing cancer or tumour, the binding  
 CC composition comprises a nucleic acid probe or primer that specifically  
 CC binds or hybridises to human or mouse IL-23p19 cDNA sequences, or the  
 CC human IL-23R sequence.

XX Sequence 2859 BP; 929 A; 575 C; 560 G; 791 T; 0 U; 4 Other;

Query Match 100.0%; Score 2857.4; DB 13; Length 2859;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2859; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 61 GGAATTATGCTCTTCAACAGCTTGAAGAGGGAACAGCTTTCTCTGCTTCAGACAT 120  
 QY 121 GAATCAAGTCACTATTCATGAGATGAGATGAGCCCTTATACATCTTCAAGCTGGT 180  
 DB 121 GAATCAAGTCACTATTCATGAGATGAGATGAGCCCTTATACATCTTCAAGCTGGT 180  
 QY 181 TCATGAGAGATTAACAATAATTAATCTGCTGACATCTGGGTGAGACACCAAT 240  
 DB 181 TCATGAGAGATTAACAATAATTAATCTGCTGACATCTGGGTGAGACACCAAT 240  
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QY 2041 GCGTTGCAATCTGAACTTGGGTTTTTCCCTGCAATAGAAATTTGCTGCTCTTTTGA 2100  
DB 2041 GCGTTGCAATCTGAACTTGGGTTTTTCCCTGCAATAGAAATTTGCTGCTCTTTTGA 2100  
QY 2101 AAAAAATGATTCACATACAAATCTTCACATGACACATGTTTCACTTCCCTTGATTA 2160  
DB 2101 AAAAAATGATTCACATACAAATCTTCACATGACACATGTTTCACTTCCCTTGATTA 2160  
QY 2161 ATACCTTAGTAGGGGATTTGCTGGCCATATGATAGCAATATGTTTCACTTACCAATCT 2220  
DB 2161 ATACCTTAGTAGGGGATTTGCTGGCCATATGATAGCAATATGTTTCACTTACCAATCT 2220  
QY 2221 TGTTTCCAGATGATGACATTTCTGTGCTCTTACATCACATGTAAGAAATCCCGGAG 2280  
DB 2221 TGTTTCCAGATGATGACATTTCTGTGCTCTTACATCACATGTAAGAAATCCCGGAG 2280  
QY 2281 CTCATGCTCTTTTAAATTTTAAAGCCATCTTCTGCTAAATTTCTTAAATTAGAATTA 2340  
DB 2281 CTCATGCTCTTTTAAATTTTAAAGCCATCTTCTGCTAAATTTCTTAAATTAGAATTA 2340  
QY 2341 GGTCCGAGAGGTGGAACATGCTTCATGTGACACATACAGGACACAAAACGACATTATGT 2400  
DB 2341 GGTCCGAGAGGTGGAACATGCTTCATGTGACACATACAGGACACAAAACGACATTATGT 2400  
QY 2401 GGAAGCCTCAGTATTTTATTAAGAGTCACTATTTCTCTTATTTTCCCTCATTTGAAA 2460  
DB 2401 GGAAGCCTCAGTATTTTATTAAGAGTCACTATTTCTCTTATTTTCCCTCATTTGAAA 2460  
QY 2461 GATGCAAAACAGCTCTCTATTTGTATGAGAAAGGTTAAATATGCAAAATACCTGTAGT 2520  
DB 2461 GATGCAAAACAGCTCTCTATTTGTATGAGAAAGGTTAAATATGCAAAATACCTGTAGT 2520  
QY 2521 AAAAAATATCTGAAAAATTTTCTTTAAATAGATCATTAGGCGAGGCTGTGTGCTCA 2580  
DB 2521 AAAAAATATCTGAAAAATTTTCTTTAAATAGATCATTAGGCGAGGCTGTGTGCTCA 2580  
QY 2581 TGCTTGAATCCAGACGCTTTGGAGCTGAGGCTGTGATCATCCTGAGGTCAAGGAT 2640  
DB 2581 TGCTTGAATCCAGACGCTTTGGAGCTGAGGCTGTGATCATCCTGAGGTCAAGGAT 2640  
QY 2641 CGAGTCAGAGCTGAGCAATATGCTGAACCCCTGCTCTACTATTAATAATTAATAATTTAGCC 2700  
DB 2641 CGAGTCAGAGCTGAGCAATATGCTGAACCCCTGCTCTACTATTAATAATTAATAATTTAGCC 2700  
QY 2701 GGGCATGTGTGAGAGGTCTTGTAAATCCAGCTACTTGTGGAGGCTGAGAGCGAGAAATCAC 2760  
DB 2701 GGGCATGTGTGAGAGGTCTTGTAAATCCAGCTACTTGTGGAGGCTGAGAGCGAGAAATCAC 2760  
QY 2761 TTGAACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2820  
DB 2761 TTGAACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2820  
QY 2821 GCAACAGAGCAAAACTCTGCTGGAATAAAAAAAAAAAAAA 2859

DB 2821 GCAACAGAGCAAAACTCTGCTGGAATAAAAAAAAAAAAAA 2859

RESULT 3  
AEA51089  
ID AEA51089 standard; DNA; 2859 BP.  
XX  
AC AEA51089;  
XX  
DT 11-AUG-2005 (first entry)  
XX  
DE Human DNAX cytokine receptor subunit 5 (DCRS5) DNA.  
XX  
KW Diagnosis; therapeutic; asthma; antiaesthetic; immune disorder;  
KW inflammation; respiratory disease; allergy; anti-allergic;  
KW chronic obstructive pulmonary disease; respiratory-gen.;  
KW pulmonary fibrosis; anti-inflammatory; pneumonia; infection;  
KW cytokine receptor family; gene; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT sig\_peptide 1..187  
FT CDS 119..2008  
FT /tag= a  
FT /tag= b  
FT /product= "Human DNAX cytokine receptor subunit 5 (DCRS5)  
FT protein"  
FT /transl\_except= (pos:125..127, aa: Xaa)  
FT /note= "Xaa corresponds to Gln or His"  
FT /transl\_except= (pos:563..565, aa: Xaa)  
FT /note= "Xaa corresponds to Gly or Arg"  
FT mat\_peptide 188..2005  
FT /tag= c  
FT /product= "Mature human DNAX cytokine receptor subunit 5  
FT (DCRS5) protein"  
PN WC2005052157-A1.  
XX  
PD 09-JUN-2005.  
XX  
PF 18-NOV-2004; 2004MO-US038886.  
XX  
PR 21-NOV-2003; 2003US-00720026.  
XX  
PA (SCHE ) SCHERING CORP.  
XX  
PI Chirica M, Kaestlein RA, Moore KW, Parham CL;  
XX  
DR WPI; 2005-418000/42.  
DR P-PSDB; AEA51090.  
XX  
PT Use of an agonist or antagonist of DNAX cytokine receptor subunit 5  
PT (DCRS5) or of p19 for treating a human subject experiencing a  
PT physiological disorder such as allergy or chronic obstructive pulmonary  
PT disorder (COPD).  
XX  
PS Claim 1; SEQ ID NO 1; 89pp; English.  
XX  
CC The present invention relates to a method of treating a human subject  
CC experiencing a physiological disorder. The method involves administering  
CC an agonist or antagonist of DNAX cytokine receptor subunit 5 (DCRS5, also  
CC known as IL-23r) or of p19, where the disorder comprises asthma or  
CC allergy, chronic obstructive pulmonary disorder (COPD) or an interstitial  
CC lung disorder. The invention is useful for treating interstitial lung  
CC disorder e.g. idiopathic pulmonary fibrosis, eosinophilic granuloma and  
CC hypersensitivity pneumonitis. The present sequence is the human DCRS5  
CC DNA.  
XX  
SQ Sequence 2859 BP; 929 A; 575 C; 560 G; 791 T; 0 U; 4 Other;  
Query Match 100.0%; Score 2857.4; DB 14; Length 2859;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2859; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGTACGGGAATTCATTTGGTTGGGACGCAACAAAGGTTGGACGCTGGCTGAAGT 60  
Db 1 GTGGTACGGGAATTCATTTGGTTGGGACGCAACAAAGGTTGGACGCTGGCTGAAGT 60  
QY 61 GGAATTATGTCTTCAACACAGGTTGAAAGAGGAAACAGTCTTTCTGCTTCCAGCAT 120  
Db 61 GGAATTATGTCTTCAACACAGGTTGAAAGAGGAAACAGTCTTTCTGCTTCCAGCAT 120  
QY 121 GAATCAAGTCACTTATCAATGGGATGCGATTAATGCCCTTTACATATCTTCAAGCTGGTG 180  
Db 121 GAATCAAGTCACTTATCAATGGGATGCGATTAATGCCCTTTACATATCTTCAAGCTGGTG 180  
QY 181 TCAATGAGGAATTAACAAATATACTGCTGCGACATCGGGGTAGAACAGCCACAAT 240  
Db 181 TCAATGAGGAATTAACAAATATACTGCTGCGACATCGGGGTAGAACAGCCACAAT 240  
QY 241 TTTTAAGATGGGTATGAAATATCTCTATATATTTGGCAAGACAAATTAGAAGTCCCAAC 300  
Db 241 TTTTAAGATGGGTATGAAATATCTCTATATATTTGGCAAGACAAATTAGAAGTCCCAAC 300  
QY 301 AAGGAACCTTCATTTTATATAAAATGGCATCAAAAGAAAGATTCAACAAAGATTA 360  
Db 301 AAGGAACCTTCATTTTATATAAAATGGCATCAAAAGAAAGATTCAACAAAGATTA 360  
QY 361 TAAACCAACAGCTCGGCTTTGGTATATAAACTTTCTGGAAACCATGCTCTATGTATCG 420  
Db 361 TAAACCAACAGCTCGGCTTTGGTATATAAACTTTCTGGAAACCATGCTCTATGTATCG 420  
QY 421 CACTGCTGAATGTCCCAACATTTTCAAGAGACACTGATATGGAAGAAACATTTCTTC 480  
Db 421 CACTGCTGAATGTCCCAACATTTTCAAGAGACACTGATATGGAAGAAACATTTCTTC 480  
QY 481 TGAATATCCGCGAGATATCTCTGATGAGTAACTGTGTCATTTATGAATATTCAGGCA 540  
Db 481 TGAATATCCGCGAGATATCTCTGATGAGTAACTGTGTCATTTATGAATATTCAGGCA 540  
QY 541 CATTGACTTGAACCTGGATGCTGGAAGCTCACTTACATAGAACAAATAACGTTGATCA 600  
Db 541 CATTGACTTGAACCTGGATGCTGGAAGCTCACTTACATAGAACAAATAACGTTGATCA 600  
QY 601 TGTGAAGAGTTTGAAGACAGAGAGAGAGACAGATATCTCACTCAAGCTATATTAACAT 660  
Db 601 TGTGAAGAGTTTGAAGACAGAGAGAGAGACAGATATCTCACTCAAGCTATATTAACAT 660  
QY 661 CTCACCTGATTCATTACAAAGGTGCAAGAGTACTTGGTTGGTCCAGACAGCAACGCG 720  
Db 661 CTCACCTGATTCATTACAAAGGTGCAAGAGTACTTGGTTGGTCCAGACAGCAACGCG 720  
QY 721 ACTTAGGCAATGGAAGAGTCAAAACAACTGCAAAATTCACCTGATATATAGTATCCTTC 780  
Db 721 ACTTAGGCAATGGAAGAGTCAAAACAACTGCAAAATTCACCTGATATATAGTATCCTTC 780  
QY 781 TGCAGCCGTCAATTTCCAGGGCTGAGACTATTAATGCTACAGTCCCAAGACATTAATTA 840  
Db 781 TGCAGCCGTCAATTTCCAGGGCTGAGACTATTAATGCTACAGTCCCAAGACATTAATTA 840  
QY 841 TTGGGATAGTCAACAAACAAATTTGAAAGGTTTCTGTGAAATGAGATACAAAGGCTACAC 900  
Db 841 TTGGGATAGTCAACAAACAAATTTGAAAGGTTTCTGTGAAATGAGATACAAAGGCTACAC 900  
QY 901 AAACCAAACTTTGGAATGTTAAAGATTTGACACCAATTTTACATATGTGCAACAGTACA 960  
Db 901 AAACCAAACTTTGGAATGTTAAAGATTTGACACCAATTTTACATATGTGCAACAGTACA 960  
QY 961 ATTCTACTTGGAGCAAACTTAAGTATGATTTCAAGTGAAGTGTCAAGAAACAGGCAA 1020  
Db 961 ATTCTACTTGGAGCAAACTTAAGTATGATTTCAAGTGAAGTGTCAAGAAACAGGCAA 1020  
QY 1021 AAGGTACTGGACGCTTGGAGTTCAACGTTTTTTCATTAACAACTGTAACAGTTCCCA 1080  
Db 1021 AAGGTACTGGACGCTTGGAGTTCAACGTTTTTTCATTAACAACTGTAACAGTTCCCA 1080

Db 1021 AAGGTACTGGACGCTTGGAGTTCAACGTTTTTTCATTAACAACTGTAACAGTTCCCA 1080  
QY 1081 GGTCAATCAAAAAGCATTTCCACATGACATAGAAATTCGGCTTAACAGTTGCTTCAT 1140  
Db 1081 GGTCAATCAAAAAGCATTTCCACATGACATAGAAATTCGGCTTAACAGTTGCTTCAT 1140  
QY 1141 CTCTACAGGGCACCTTACTTCTGACAAACAGAGAGACATTTGACCTTTATTTGGGAATGAT 1200  
Db 1141 CTCTACAGGGCACCTTACTTCTGACAAACAGAGAGACATTTGACCTTTATTTGGGAATGAT 1200  
QY 1201 CGTCTTGCTGTATGTGTCAATTCCTTCTTTGATTTGGGAATTTAACAGATCATTTCCG 1260  
Db 1201 CGTCTTGCTGTATGTGTCAATTCCTTCTTTGATTTGGGAATTTAACAGATCATTTCCG 1260  
QY 1261 AACTGGGATTTAAAGAGATCTTATGTTAATACCAAGTGGCTTTATGAAGATATTC 1320  
Db 1261 AACTGGGATTTAAAGAGATCTTATGTTAATACCAAGTGGCTTTATGAAGATATTC 1320  
QY 1321 TAATATGAAAAACAGCAATGTTGTGAAAAATGCTACAGAAAAATGTGAATTA 1380  
Db 1321 TAATATGAAAAACAGCAATGTTGTGAAAAATGCTACAGAAAAATGTGAATTA 1380  
QY 1381 TAATTCAGTGAAGAGTCTCTATATGTTGATCCATGATTAACAGAGATTAAGAAATCTT 1440  
Db 1381 TAATTCAGTGAAGAGTCTCTATATGTTGATCCATGATTTACAGAGATTAAGAAATCTT 1440  
QY 1441 CATCCAGAACACAGACCTTACAGACTACAGAGAGAAATACAGACCCCTGGAGACAAG 1500  
Db 1441 CATCCAGAACACAGACCTTACAGACTACAGAGAGAAATACAGACCCCTGGAGACAAG 1500  
QY 1501 AGACTACCGGCAAACTCGCTATTTGCAAAATCTACAGTTGTATATATTCCTGATCTCA 1560  
Db 1501 AGACTACCGGCAAACTCGCTATTTGCAAAATCTACAGTTGTATATATTCCTGATCTCA 1560  
QY 1561 CACTGATATTAACCCCAATTTTCAAAATTTTCTGCTGAGGAGAGCACTCAGCAATTA 1620  
Db 1561 CACTGATATTAACCCCAATTTTCAAAATTTTCTGCTGAGGAGAGCACTCAGCAATTA 1620  
QY 1621 TAATGAATAATTAATCTTCTTAACACTTAACCAACAGTGAATTCCTTAGACTCAGAAATTA 1680  
Db 1621 TAATGAATAATTAATCTTCTTAACACTTAACCAACAGTGAATTCCTTAGACTCAGAAATTA 1680  
QY 1681 TCCAGGTTACAAAAGCATCTTAATTTGCTTTTCTGTTCAAGTGTGAATTCACCTAC 1740  
Db 1681 TCCAGGTTACAAAAGCATCTTAATTTGCTTTTCTGTTCAAGTGTGAATTCACCTAC 1740  
QY 1741 CAACACAAATTTCTTGGAGAAATTAAGCCATTAATTAATCAAGAGAAATGCAGTCTCC 1800  
Db 1741 CAACACAAATTTCTTGGAGAAATTAAGCCATTAATTAATCAAGAGAAATGCAGTCTCC 1800  
QY 1801 TGAATACAAAACCTCAGTGAAGAGAGAAACCAACATGCTTTTGGAAATGATTCACCCAG 1860  
Db 1801 TGAATACAAAACCTCAGTGAAGAGAGAAACCAACATGCTTTTGGAAATGATTCACCCAG 1860  
QY 1861 TGAATCTATTCCAGAACAGACCTGCTTCTGTAGAAATTTGTTCTGTTTGGGAAATCGT 1920  
Db 1861 TGAATCTATTCCAGAACAGACCTGCTTCTGTAGAAATTTGTTCTGTTTGGGAAATCGT 1920  
QY 1921 GAATGAGAGTGGCATCTATTAATCTTATTTTCCACAAAATATTTTGGAAAGCCACTT 1980  
Db 1921 GAATGAGAGTGGCATCTATTAATCTTATTTTCCACAAAATATTTTGGAAAGCCACTT 1980  
QY 1981 CAATGAGATTTCACTCTGGAAGAAAGTGAAGCTGTGTGTCAAAATCAATGTAGAAAGCT 2040  
Db 1981 CAATGAGATTTCACTCTGGAAGAAAGTGAAGCTGTGTGTCAAAATCAATGTAGAAAGCT 2040  
QY 2041 GCCTTGCAATCTGAACCTTGGGTTTTCTGTGCAATAGAAATTTGAATTTCTGTTTTGA 2100  
Db 2041 GCCTTGCAATCTGAACCTTGGGTTTTCTGTGCAATAGAAATTTGAATTTCTGTTTTGA 2100  
QY 2101 AAAAAATGATTTCACTACATCAAAATCTTCACTGACACATGTTTTCATTTCCCTTGGATTA 2160  
Db 2101 AAAAAATGATTTCACTACATCAAAATCTTCACTGACACATGTTTTCATTTCCCTTGGATTA 2160

Qy	2161	ATACCTAGTGGGGATGTCGGGCGATATGATAGCAATATGTTTCAGTCTACCAATCT	2220
Dp	2161	ATACCTAGTAGGGGATGTGGGCCATATGATATGATATGATTTCACTTACCAATCT	2220
Qy	2221	TGTTTCCAGATGATGACATTTCTGTGCTCTACCATCAGCATGTAAAGATTTCCGGAG	2280
Dp	2221	TGTTTCCAGATGATGACATTTCTGTGCTCTACCATCAGCATGTAAAGATTTCCGGAG	2280
Qy	2281	CTCCATGCTTTTATTTATTTAGCCATCTTCTGCCMAATTTCTTAAATTAGAAATTAA	2340
Dp	2281	CTCCATGCTTTTATTTATTTAGCCATCTTCTGCCMAATTTCTTAAATTAGAAATTAA	2340
Qy	2341	GGTCCCGAAGGTGAAACAATGCTTACATGGTCAACATACAGGCACAAAACAGCATTTAGT	2400
Dp	2341	GGTCCCGAAGGTGAAACAATGCTTACATGGTCAACATACAGGCACAAAACAGCATTTAGT	2400
Qy	2401	GGAGCCCTCATGTATTTTATAGAGTAACTATTTCTCTTATTTTCCCTCATTTGAA	2460
Dp	2401	GGAGCCCTCATGTATTTTATAGAGTAACTATTTCTCTTATTTTCCCTCATTTGAA	2460
Qy	2461	GATGCAAAACAGCTCTCATTTGTGTACAGAAAGGTAATAATATGCAAAATACCTGGTAGT	2520
Dp	2461	GATGCAAAACAGCTCTCATTTGTGTACAGAAAGGTAATAATATGCAAAATACCTGGTAGT	2520
Qy	2521	AAATATAATGCTGAAAAATTTTCTTTAAATATAGATCATTTGGCCAGGCGTGTGGCTCA	2580
Dp	2521	AAATATAATGCTGAAAAATTTTCTTTAAATATAGATCATTTGGCCAGGCGTGTGGCTCA	2580
Qy	2581	TGCTTTGTATCCACGACCTTTGGTAGAGGTGAGGTGATCACTGAGGTCAAGAGTT	2640
Dp	2581	TGCTTTGTATCCACGACCTTTGGTAGAGGTGAGGTGATCACTGAGGTCAAGAGTT	2640
Qy	2641	CGAGTCCAGCGCTGGCCATATATGCTGAAACCTGTCTCTATCTAAATATTCAAAAATTAGCC	2700
Dp	2641	CGAGTCCAGCGCTGGCCATATATGCTGAAACCTGTCTCTATCTAAATATTCAAAAATTAGCC	2700
Qy	2701	GGCCATGGTGGCAGGTGCTTGTAAATCCAGCTACTTGGGAGGCTGAGGACAGAGAAATCAC	2760
Dp	2701	GGCCATGGTGGCAGGTGCTTGTAAATCCAGCTACTTGGGAGGCTGAGGACAGAGAAATCAC	2760
Qy	2761	TTGAAACCGAAGGACAGAGGTGACCTGAGCTGAGATTTGTGCCACTGCCAGCCTGG	2820
Dp	2761	TTGAAACCGAAGGACAGAGGTGACCTGAGCTGAGATTTGTGCCACTGCCAGCCTGG	2820
Qy	2821	GCAACAAAGACAAAACTCTGTCTGGAAAAAATTTTAAAAA	2859
Dp	2821	GCAACAAAGACAAAACTCTGTCTGGAAAAAATTTTAAAAA	2859
RESULT 4			
AAD38773			
ID	AAD38773 standard; cDNA, 2830 BP.		
XX	AAD38773;		
AC	23-SBP-2002 (first entry)		
XX	Human haematopoietin receptor 2 (HPR2) cDNA.		
DE	Human; haematopoietin receptor; receptor; HPR1, HPR2; cell proliferation;		
KM	pancytopenia; leukopenia; anaemia; thrombocytopenia; osteoporosis;		
KM	neurodegenerative disorder; leukemia; carcinoma; haematologic disorder;		
KM	cancer; myelodysplastic syndrome; idiopathic thrombocytopenic purpura;		
KM	ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;		
KM	osteoclast disorder; peridontitis; acute polyneuropathy; Bell's palsy;		
KM	anorexia nervosa; chronic fatigue syndrome; Creutzfeldt-Jacob disease;		
KM	demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;		
KM	vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;		
KM	stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;		
KM	ischaemic disease; gene; se.		
XX	Homo sapiens		
DS			

XX	Key	Location/Qualifiers
PH	107. .1996	
FT	CD5	
XX		
FT		/product= "Human HPR2 protein"
FT		/tag= a
FT		/note= "This region is specifically claimed as SEQ ID NO: 20 in claim 9 of the specification"
FT		137. .175
FT	sig_peptide	
FT		/tag= b
FT	mat_peptide	
FT		/tag= c
FT		/product= "Human mature HPR2 protein"
FT		replace(1035, c)
FT	variation	
FT		/tag= d
FT		replace(2172, G)
FT		/tag= e
XX		
PN	WO200229060-A2.	
XX		
XX	11-APR-2002.	
PD		
XX		
PF	05-OCT-2001; 2001WO-US031634.	
XX		
PR	06-OCT-2000; 2000US-0238706P.	
PR	13-OCT-2000; 2000US-0240476P.	
PR	20-FEB-2001; 2001US-0270282P.	
XX		
PA	(IMMV ) IMMUNEX CORP.	
PI	Coeman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR;	
XX		
DR	WPI; 2002-330172/36.	
XX	P-PSDB; AAE24033.	
PT		
PT	Human and murine hematopoietin receptor polypeptides HPR1 and HPR2,	
PT	useful for treating cell proliferation, metabolic, and reproductive	
PT	hormone related conditions.	
XX		
PS	Claim 9; Page 117-119; 136pp; English.	
XX		
CC	The present invention relates to human and murine haematopoietin receptor	
CC	polypeptides HPR1 and HPR2. Sequences of the invention are useful for	
CC	treating cell proliferation conditions e.g., pancytopenia, leukopaenia,	
CC	anemia, thrombocytopaenia, neurodegenerative disorders and osteoporosis	
CC	resulting from a lack of bone-forming cells. They are also useful for	
CC	treating cell proliferation conditions such as leukaemia and tumour	
CC	metastasis, osteoporosis resulting from an excess of bone-resorbing	
CC	cells. HPR sequences are also useful for treating medical conditions and	
CC	diseases such as cell proliferation, metabolic and reproductive hormone	
CC	related conditions. They are useful for treating various haematologic and	
CC	oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal	
CC	carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell,	
CC	cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including	
CC	cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma,	
CC	sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer),	
CC	squamous cell carcinoma), haematologic disorders, anaemias (e.g., anaemia	
CC	of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelo-	
CC	dysplastic syndromes (including refractory anaemia, refractory anaemia	
CC	with ringed sideroblasts or with excess blasts), idiopathic thrombocyto-	
CC	penic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/	
CC	myeloid metaplasia, osteoclast disorders that lead to bone loss such as	
CC	osteoporosis including post-menopausal osteoporosis, periodontitis	
CC	resulting in tooth loosening or loss, prosthesis loosening after joint	
CC	replacement, neurodegenerative conditions (e.g., acute polymyopathy,	
CC	Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible	
CC	dementia including Creutzfeldt-Jacob disease, demyelinating neuropathy,	
CC	Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome,	
CC	myasthenia gravis, chronic neuronal degeneration, stroke including	
CC	cerebral ischaemic diseases. HPR1 and HPR2 polypeptides are also useful	
CC	for treating various other disorders such as osteoporosis, obesity,	
CC	deficient mammary development and infertility. The present sequence is	
XX	human HPR1 cDNA	
XX		

SQ Sequence 2830 BP; 922 A; 574 C; 551 G; 783 T; 0 U; 0 Other;  
Query Match 98.3%; Score 2810.2; DB 6; Length 2830;  
Best local Similarity 99.8%; Pred. No. 0;  
Matches 2809; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 28 CAGCCACAAAGGCTGGAGCCCTGCTGTAAGTGAATTATGTGCTTCAAAACAGTTGAA 87  
DB 16 CAGCCACAAAGGCTGGAGCCCTGCTGTAAGTGAATTATGTGCTTCAAAACAGTTGAA 75  
QY 88 AGAGGGAAAAGCTTTTCTGCTTCAGACATGAATCAGTCACTATTCCTTCAAGGATGC 147  
DB 76 AGAGGGAAAAGCTTTTCTGCTTCAGACATGAATCAGTCACTATTCCTTCAAGGATGC 135  
QY 148 AGAATAGCCCTTACATACCTTTCAGCTGTGTGATGAGAAATTAACAATATTAACCTG 207  
DB 136 AGAATAGCCCTTACATACCTTTCAGCTGTGTGATGAGAAATTAACAATATTAACCTG 195  
QY 208 CTCTGGCCACATCTGGGTAGAACCCAGCCACAATTTTTTAAGATGGGTATGAAATCTCTAT 267  
DB 196 CTCTGGCCACATCTGGGTAGAACCCAGCCACAATTTTTTAAGATGGGTATGAAATCTCTAT 255  
QY 268 ATATTCGCAAGCAGCAATTAAGAACTGCCCAACCAAGGAAACCTTCAATTTATATTAATG 327  
DB 256 ATATTCGCAAGCAGCAATTAAGAACTGCCCAACCAAGGAAACCTTCAATTTATATTAATG 315  
QY 328 CATCAAGAAAGATTTCAATTCACAAGATTTAATAAACAACAGCTCGCTTTGTATTA 387  
DB 316 CATCAAGAAAGATTTCAATTCACAAGATTTAATAAACAACAGCTCGCTTTGTATTA 375  
QY 388 AAACTTTCTGGAACACATCTCTATATGACTGCACTGTGAATGTCCCAACATTTTCA 447  
DB 376 AAACTTTCTGGAACACATCTCTATATGACTGCACTGTGAATGTCCCAACATTTTCA 435  
QY 448 AGAGACCTGATATGTGGAAAAAGACATTTCTTCGTGATATCCCGACATATTCCTGATGA 507  
DB 436 AGAGACCTGATATGTGGAAAAAGACATTTCTTCGTGATATCCCGACATATTCCTGATGA 495  
QY 508 AGTAACCTGTGTATTTATGATATTTACAGCAACATGACTTGCACTGGAATCTTGGAA 567  
DB 496 AGTAACCTGTGTATTTATGATATTTACAGCAACATGACTTGCACTGGAATCTTGGAA 555  
QY 568 GCTCACCTACATAGACAAATAATCTGTGTACATGTGAAGATTTAGAGACAGAAAGAA 627  
DB 556 GCTCACCTACATAGACAAATAATCTGTGTACATGTGAAGATTTAGAGACAGAAAGAA 615  
QY 628 GCAACGATACCTACCTCAAGCTATATTAACATCTCCACGATTCATTAAGAGTGCA 687  
DB 616 GCAACGATACCTACCTCAAGCTATATTAACATCTCCACGATTCATTAAGAGTGCA 675  
QY 688 GAAGTACTTGGTTGGTCCAGCAGCAAGCACTAGAGCATGGAAGTCAAAACAACCT 747  
DB 676 GAAGTACTTGGTTGGTCCAGCAGCAAGCACTAGAGCATGGAAGTCAAAACAACCT 735  
QY 748 GCAAAATTCACCTGGATATATAGTATACCTTTCGACCGGTCAATTTCCAGGCTGAGAC 807  
DB 736 GCAAAATTCACCTGGATATATAGTATACCTTTCGACCGGTCAATTTCCAGGCTGAGAC 795  
QY 808 TATTAATGCTACAGTGGCCCAAGCAATAATTTATGGGATAGTCAAAACAATTTGAAA 867  
DB 796 TATTAATGCTACAGTGGCCCAAGCAATAATTTATGGGATAGTCAAAACAATTTGAAA 855  
QY 868 GGTTCCTGTGAATGAGATCAAGGCTACACAAACCAAACTTGAATGTAAAGAAAT 927  
DB 856 GGTTCCTGTGAATGAGATCAAGGCTACACAAACCAAACTTGAATGTAAAGAAAT 915  
QY 928 TGAACACCAATTTTACATATGTGCAACAGTCAAAATTTCTACTTGGAGCCAAACATTAAGTA 987  
DB 916 TGAACACCAATTTTACATATGTGCAACAGTCAAAATTTCTACTTGGAGCCAAACATTAAGTA 975  
QY 988 CGATTTTCAAGTGAAGTGAAGAAACAGGCAAAAGGTACTGGACGCTTGGAGTTCACT 1047  
DB 976 CGATTTTCAAGTGAAGTGAAGAAACAGGCAAAAGGTACTGGACGCTTGGAGTTCACT 1035

QY 1048 GTTTTTCATTAACAACCTGAAACAGTTCCTCCAGGTCAATCAAAAGCATTTCCACATGA 1107  
DB 1036 GTTTTTCATTAACAACCTGAAACAGTTCCTCCAGGTCAATCAAAAGCATTTCCACATGA 1095  
QY 1108 CACATGAATTCGGGCTAAACAGTTCCTTCATCTCTACAGGGCACCCTTAATCTTCACAA 1167  
DB 1096 CACATGAATTCGGGCTAAACAGTTCCTTCATCTCTACAGGGCACCCTTAATCTTCACAA 1155  
QY 1168 CAGAGAGACATTTGACTTTTATTTGGGAATGATCGTCTTTCGTATATGTGCAATTCCT 1227  
DB 1156 CAGAGAGACATTTGACTTTTATTTGGGAATGATCGTCTTTCGTATATGTGCAATTCCT 1215  
QY 1228 TTCTTTGATGGGATATTTAAACAGATCATTCGAACTGGGATTTAAAGAAAGATCTTAT 1287  
DB 1216 TTCTTTGATGGGATATTTAAACAGATCATTCGAACTGGGATTTAAAGAAAGATCTTAT 1275  
QY 1288 GTTAATACCAAGTGGCTTTATGAAATATTCCTTAATATGAAAAACAGCAATGTGTGA 1347  
DB 1276 GTTAATACCAAGTGGCTTTATGAAATATTCCTTAATATGAAAAACAGCAATGTGTGA 1335  
QY 1348 AATGCTACAGAAATATGAACTTATGAAATTAATTCAGTGAACAGTCTCATATGT 1407  
DB 1336 AATGCTACAGAAATATGAACTTATGAAATTAATTCAGTGAACAGTCTCATATGT 1395  
QY 1408 TGAATCCATGATTTACAGAGATTAAGAAATCTTCATCCAGAAACACAGCTTACAGATA 1467  
DB 1396 TGAATCCATGATTTACAGAGATTAAGAAATCTTCATCCAGAAACACAGCTTACAGATA 1455  
QY 1468 CAAAGAGGAATATACAGACCCCTGGAGACAAGAGCTACCCGCAAAACCTGGTATTTGA 1527  
DB 1456 CAAAGAGGAATATACAGACCCCTGGAGACAAGAGCTACCCGCAAAACCTGGTATTTGA 1515  
QY 1528 CAATACAGTGTATATATTCCTGATCTCAACATCTGATATTAACCCCAATTTCAAA 1587  
DB 1516 CAATACAGTGTATATATTCCTGATCTCAACATCTGATATTAACCCCAATTTCAAA 1575  
QY 1588 TTTTCTGCTGAGGAAGCCATCTCAGCAATTAATTAAGAAATTAATCTTCAACCTTAA 1647  
DB 1576 TTTTCTGCTGAGGAAGCCATCTCAGCAATTAATTAAGAAATTAATCTTCAACCTTAA 1635  
QY 1648 ACCACAGTTGATTCCTTACAGCAATTAATTCAGAGTTTACAAACAGCTCTTAATTT 1707  
DB 1636 ACCACAGTTGATTCCTTACAGCAATTAATTCAGAGTTTACAAACAGCTCTTAATTT 1695  
QY 1708 TGTCTTTCTGTTCAGTGTGAATCACTAAGCAACAATAATTTCTTGGAAATTTAAG 1767  
DB 1696 TGTCTTTCTGTTCAGTGTGAATCACTAAGCAACAATAATTTCTTGGAAATTTAAG 1755  
QY 1768 CCTCATATTAATCAAGAGAAATGCAATCTCCTGACATACAAACTCAGTGAAGAGGA 1827  
DB 1756 CCTCATATTAATCAAGAGAAATGCAATCTCCTGACATACAAACTCAGTGAAGAGGA 1815  
QY 1828 AACCAACAGCTTTTGGAAAAATGATTCACCCAGTGAACATATTCAGAAACAGACCTGCT 1887  
DB 1816 AACCAACAGCTTTTGGAAAAATGATTCACCCAGTGAACATATTCAGAAACAGACCTGCT 1875  
QY 1888 TCCGTGAATTTGTCTCTGTTTGGGGATCGTGAATGAGAGTTCCTATTAATATAC 1947  
DB 1876 TCCGTGAATTTGTCTCTGTTTGGGGATCGTGAATGAGAGTTCCTATTAATATAC 1935  
QY 1948 TTAATTTCCAAAAATATTTTGGAAAACCACTTCAATAGATTTCACTTGGAAAAGTA 2007  
DB 1936 TTAATTTCCAAAAATATTTTGGAAAACCACTTCAATAGATTTCACTTGGAAAAGTA 1995  
QY 2008 GAGCTGTGTGTCAAAATCAATTAAGAAAGCTGCTTGCATCTGAACCTTGGGTTTTC 2067  
DB 1996 GAGCTGTGTGTCAAAATCAATTAAGAAAGCTGCTTGCATCTGAACCTTGGGTTTTC 2055  
QY 2068 CTGCAATTAAGAAATTTGAAATCTGTCTTTTGAATAAATATGATTCATACAAATCTTC 2127  
DB 2056 CTGCAATTAAGAAATTTGAAATCTGTCTTTTGAATAAATATGATTCATACAAATCTTC 2115

QY 2128 ACATGACACATGTTTCTATTTCCCTTGATTAATACTAGAGGAGATGCTGGCCA 2187  
DB 2116 ACATGACACATGTTTCTATTTCCCTTGATTAATACTAGAGGAGATGCTGGCCA 2175  
QY 2188 TAATGATAGATATGTTTCAAGTTCTACCAATCTTTGTTCCAGAGTATGACATTTCTGTG 2247  
DB 2176 TAATGATAGATATGTTTCAAGTTCTACCAATCTTTGTTCCAGAGTATGACATTTCTGTG 2235  
QY 2248 CTCCTACCATCACATGTAAGAAATTCGGGAGCTCCATGCTTTTAATTTAGCCATT 2307  
DB 2236 CTCCTACCATCACATGTAAGAAATTCGGGAGCTCCATGCTTTTAATTTAGCCATT 2295  
QY 2308 CTTCTGCTTATTTCTTAAATTAAGAAATTAAGTCCCAAGGTGAAATGCTTCATG 2367  
DB 2296 CTTCTGCTTATTTCTTAAATTAAGAAATTAAGTCCCAAGGTGAAATGCTTCATG 2355  
QY 2368 GTCAACATACAGGACACAAAACAGCATTAATGAGAGCTCATGATTTTATATAGT 2427  
DB 2356 GTCAACATACAGGACACAAAACAGCATTAATGAGAGCTCATGATTTTATATAGT 2415  
QY 2428 CAATATTTCTCTTATTTTCCCTCATGAAAGATGCAAAACAGCTCTCATTTGTGATC 2487  
DB 2416 CAATATTTCTCTTATTTTCCCTCATGAAAGATGCAAAACAGCTCTCATTTGTGATC 2475  
QY 2488 AGAAGGGTAAATTAATGCAAAATACCTGTATGTAATAATATGCTGAAAATTTCTTTA 2547  
DB 2476 AGAAGGGTAAATTAATGCAAAATACCTGTATGTAATAATATGCTGAAAATTTCTTTA 2535  
QY 2548 AAATAGATATTAAGGACAGGCGGTGTGCTCATGCTTTGTAATCCAGCATTTGTGATG 2607  
DB 2536 AAATAGATATTAAGGACAGGCGGTGTGCTCATGCTTTGTAATCCAGCATTTGTGATG 2595  
QY 2608 CTGAGGTGGTGTGATCACTGAGGTGCAAGGTTGCAAGTCCAGCTGCAATATGCTGAA 2667  
DB 2596 CTGAGGTGGTGTGATCACTGAGGTGCAAGGTTGCAAGTCCAGCTGCAATATGCTGAA 2655  
QY 2668 ACCCTGCTCTTAAATTAATGCAAAATTAAGCGGCGCATGATGTCAGATTC 2727  
DB 2656 ACCCTGCTCTTAAATTAATGCAAAATTAAGCGGCGCATGATGTCAGATTC 2715  
QY 2728 CAGCTACTGGAGGCTGAGGAGGAGAAATCACTTGAACAGAGGCAAGAGTTGCACT 2787  
DB 2716 CAGCTACTGGAGGCTGAGGAGGAGAAATCACTTGAACAGAGGCAAGAGTTGCACT 2775  
QY 2788 GAGCTAGATTTGGCCATGCACTCCAGCTGGGCAACAAGAAATCTCTGTC 2842  
DB 2776 GAGCTAGATTTGGCCATGCACTCCAGCTGGGCAACAAGAAATCTCTGTC 2830

RESULT 5  
AA87820  
ID AAF87820 standard; cDNA; 2123 BP.  
XX AAF87820;  
AC  
XX  
XX  
DT 11-JUL-2001 (first entry)

DE Human haemopoietin receptor protein NR12.3 encoding cDNA SEQ ID NO:5.  
XX  
XX Human haemopoietin receptor protein; NR12; immunosuppressive;  
KW anti-allelic; haemopoietin factor; autoimmune disease; tissue rejection;  
KM metal allergy; pollen allergy; ss.  
XX  
OS Homo sapiens.

XX Key Location/Qualifiers  
FH 98.1987  
FT CDS  
FT /tag= a  
FT /product= "NR12.3"  
FT /note= "haemopoietin receptor protein"  
XX  
XX

MO200123556-A1.

PD 05-APR-2001.  
XX  
XX 27-SEP-2000; 2000MO-JP006654.  
XX  
XX 27-SEP-1999; 99JP-00273358.  
PR 03-AUG-2000; 2000JP-00240397.  
XX  
XX (CHUGAI) CHUGAI RES INST MOLECULAR MEDICINE INC.  
PA  
PI Maeda M, Yaguchi N;  
XX  
XX WPI, 2001-266154/27.  
DR P-PSDB; AAB74965.  
XX  
XX New hemopoietin receptor protein NR12 useful for screening for new  
PT binding factors for potential treatment of autoimmune disease, tissue  
PT rejection and allergies.  
XX  
XX Claim 1; Fig 6; 140pp; Japanese.  
XX  
XX The present sequence encodes a human haemopoietin receptor protein NR12  
CC designated NR12.3. NR12 has immunosuppressive and anti-allelic  
CC activities. NR12 can be used for searching for haemopoietin factors with  
CC the potential for controlling autoimmune disease, tissue rejection and  
CC allergies against e.g. metals and pollen  
XX  
XX Sequence 2123 BP; 731 A; 419 C; 395 G; 578 T; 0 U; 0 Other;

Query Match 72.8%; Score 2081.4; DB 5; Length 2123;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 2085; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 28 CAGCCAAACAAGGGTGGAGCGCTGCTGAAGGAAATATGCTTCAAAAGGTTGAA 87  
DB 7 CAGCCAAACAAGGGTGGAGCGCTGCTGAAGGAAATATGCTTCAAAAGGTTGAA 66  
QY 88 AGAGGGAACAGCTCTTCTGCTTCAGACATGAATCAAGTCAATTCATGGAATGC 147  
DB 67 AGAGGGAACAGCTCTTCTGCTTCAGACATGAATCAAGTCAATTCATGGAATGC 126  
QY 148 AGTAATAGCCCTTTAATCACTCTTCAGCTGCTCATGAGAAATTAATAATGCTG 207  
DB 127 AGTAATAGCCCTTTAATCACTCTTCAGCTGCTCATGAGAAATTAATAATGCTG 186  
QY 208 CTCTGGCCATCTGGGTGGAACCAAGCAATTTTAAGATGGATATCTCTAT 267  
DB 187 CTCTGGCCATCTGGGTGGAACCAAGCAATTTTAAGATGGATATCTCTAT 246  
QY 268 ATATGCAAGCAGCAATTAAGAACTGCCAACAGAAATTCATTTTATATAAATG 327  
DB 247 ATATGCAAGCAGCAATTAAGAACTGCCAACAGAAATTCATTTTATATAAATG 306  
QY 328 CATCAAGAAAGATTTCAATCAACAAGATTAATAAACAAGCTGGCTTTGTATTA 387  
DB 307 CATCAAGAAAGATTTCAATCAACAAGATTAATAAACAAGCTGGCTTTGTATTA 366  
QY 388 AAACCTTGGGAACCAAGCTCTTATGATGCACTGCTGAATGCCCCAATTTTCA 447  
DB 367 AAACCTTGGGAACCAAGCTCTTATGATGCACTGCTGAATGCCCCAATTTTCA 426  
QY 448 AGAGACATGATATGGAAGAAAGCAATTTCTTGTGATATCCCGCAGATATTCCTGATGA 507  
DB 427 AGAGACATGATATGGAAGAAAGCAATTTCTTGTGATATCCCGCAGATATTCCTGATGA 486  
QY 508 AGTAACCTGTGTATTTATGATATTTCAAGCAACATGACTTGCAATCTGGAATCTGGA 567  
DB 487 AGTAACCTGTGTATTTATGATATTTCAAGCAACATGACTTGCAATCTGGAATCTGGA 546  
QY 568 GCTCACCTCATATGACACAAAATAGGTGGAATGTAAGAGTTTGAAGACAGAAAGA 627  
DB 547 GCTCACCTCATATGACACAAAATAGGTGGAATGTAAGAGTTTGAAGACAGAAAGA 606  
QY 628 GCAACAGTATCTCACTCAAGCTATATTAATCTCACTGATTCATTAAGGTGCA 687



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Db      607 GCAACGATATCTCACTCAAGCTATATTAATCATCTCACTGATTCATTAACAGGTGCAA 666
Qy      688 GAAGTCTTGTTGGGTCCAGAGCAACGCACTGAGCAGAGAGTCAAAACAAT 747
Db      667 GAAGTCTTGTTGGGTCCAGAGCAACGCACTGAGCAGAGAGTCAAAACAAT 726
Qy      748 GCAATTCACCTGATGATATAGTATACCTTCTGACGCGTCAATTTCCAGGCGTGAAC 807
Db      727 GCAATTCACCTGATGATATAGTATACCTTCTGACGCGTCAATTTCCAGGCGTGAAC 786
Qy      808 TATTAATGCTACAGTCCCAAGACCAATATTTATTTGGGATAGTCAAAACAATTTGAAA 867
Db      787 TATTAATGCTACAGTCCCAAGACCAATATTTATTTGGGATAGTCAAAACAATTTGAAA 846
Qy      868 GGTTCCTGGAATGAGATACAGAGCTACAAACAACCAACTGGATGTTAAAGATT 927
Db      847 GGTTCCTGGAATGAGATACAGAGCTACAAACAACCAACTGGATGTTAAAGATT 906
Qy      928 TGAACCAATTTTACATATGTGCAACAGTCAAAATTTCTACTGGAGCCAAACAATTAAATA 987
Db      907 TGAACCAATTTTACATATGTGCAACAGTCAAAATTTCTACTGGAGCCAAACAATTAAATA 966
Qy      988 CGATTTTCAAGTGAATGTCAAGAAACAGGCAAAAGGTACTGGAGCTTGAAGTTCAAC 1047
Db      967 CGATTTTCAAGTGAATGTCAAGAAACAGGCAAAAGGTACTGGAGCTTGAAGTTCAAC 1026
Qy      1048 GTTTTTCATTAACACCTGAAAACAGTTCCCGAGGTGACATCAAAAGCATTTCCAAACATGA 1107
Db      1027 GTTTTTCATTAACACCTGAAAACAGTTCCCGAGGTGACATCAAAAGCATTTCCAAACATGA 1086
Qy      1108 CACATGAAATTCGAGGCTAAACAGTTCCTCATCTCTACAGGCACTTACTTGACAA 1167
Db      1087 CACATGAAATTCGAGGCTAAACAGTTCCTCATCTCTACAGGCACTTACTTGACAA 1146
Qy      1168 CAGAGGAGCATTTGGAATTTTATTTGGGAATGATGCTTTTGGTATATGTTTCAATTC 1227
Db      1147 CAGAGGAGCATTTGGAATTTTATTTGGGAATGATGCTTTTGGTATATGTTTCAATTC 1206
Qy      1228 TTCTTTGATTTGGGATATTTTAAACAGATCAATTCGAACTGGGATTTAAAGAAAGATCTAAT 1287
Db      1207 TTCTTTGATTTGGGATATTTTAAACAGATCAATTCGAACTGGGATTTAAAGAAAGATCTAAT 1266
Qy      1288 GTTAATACCAAGTGGCTTTATGAGATATTCCTAATATGAAAACAGCATGTGTGAA 1347
Db      1267 GTTAATACCAAGTGGCTTTATGAGATATTCCTAATATGAAAACAGCATGTGTGAA 1326
Qy      1348 AATGCTACAGGAAATATGTAATTTATGATTAATTAATTTCCAGTGAAGAGTCTTATATGT 1407
Db      1327 AATGCTACAGGAAATATGTAATTTATGATTAATTAATTTCCAGTGAAGAGTCTTATATGT 1386
Qy      1408 TGATCCCATATTTACAGAGATTAAGAAATCTTCATCCGAAACAAGGCTACAGACTA 1467
Db      1387 TGATCCCATATTTACAGAGATTAAGAAATCTTCATCCGAAACAAGGCTACAGACTA 1446
Qy      1468 CAAGAAAGAAATACAGAGCCCTGAGACAAGAGACTAACCCGAAAATCGTATTCGA 1527
Db      1447 CAAGAAAGAAATACAGAGCCCTGAGACAAGAGACTAACCCGAAAATCGTATTCGA 1506
Qy      1528 CAATPACTACAGTGTATATATTCCTGATCTCAACAGTGAATTAACCCCAATTTCAA 1587
Db      1507 CAATPACTACAGTGTATATATTCCTGATCTCAACAGTGAATTAACCCCAATTTCAA 1566
Qy      1588 TTTTTCGCGCAGAGGAAGCAATCGACATTAATTAAGAAATTAATCTCTTAACACTTA 1647
Db      1567 TTTTTCGCGCAGAGGAAGCAATCGACATTAATTAAGAAATTAATCTCTTAACACTTA 1626
Qy      1648 ACCACAGTGAATCTCTTAGACTCAGAAATTAATCCAGGTTACAAAGAGATCTAATTT 1707
Db      1627 ACCACAGTGAATCTCTTAGACTCAGAAATTAATCCAGGTTACAAAGAGATCTAATTT 1686
Qy      1708 TGCCTTTTCTGTTTCAAGTGTGAATTCATGAGACACAAATTTTCTTGAGAAATTAAG 1767

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Db      1687 TGCCTTTTCTGTTTCAAGTGTGAATTCATTAAGCAACAAATATTTCTTGAGAAATTAAG 1746
Qy      1768 CTTCAATATTAATTCAGAGAAATGCAATTCCTGACATACAAAACTCAGTAGAGAGGA 1827
Db      1747 CTTCAATATTAATTCAGAGAAATGCAATTCCTGACATACAAAACTCAGTAGAGAGGA 1806
Qy      1828 AACCAACATGCTTTTGGAAAATGATTCACCCAGTGAATCTATTCAGAAACAGCCCTGCT 1887
Db      1807 AACCAACATGCTTTTGGAAAATGATTCACCCAGTGAATCTATTCAGAAACAGCCCTGCT 1866
Qy      1888 TCCGTATGAATTTGTCTCCCTGTTGGGGAAATCGGAATGAGAGAGTTCATTAATAC 1947
Db      1867 TCCGTATGAATTTGTCTCCCTGTTGGGGAAATCGGAATGAGAGAGTTCATTAATAC 1926
Qy      1948 TTATTTTCCAAATAATTTTGGAAAAGCACTTCAATAGATTTCACTTTGAAAAAGTA 2007
Db      1927 TTATTTTCCAAATAATTTTGGAAAAGCACTTCAATAGATTTCACTTTGAAAAAGTA 1986
Qy      2008 GAGCTGTGCTCAAAATTCATATGAGAAAGCTGCTTGCAATCTGAACCTTGAGTTTCC 2067
Db      1987 GAGCTGTGCTCAAAATTCATATGAGAAAGCTGCTTGCAATCTGAACCTTGAGTTTCC 2046
Qy      2068 CTGCAATGAGAAATTTGAAATTCCTCTTTTGAATAAATGTAATGACATACAAA 2122
Db      2047 CTGCAATGAGAAATTTGAAATTCCTCTTTTGAATAAATGTAATGACATACAAA 2101

RESULT 6
AAF87822
ID AAF87822 standard; cDNA, 1910 BP.
XX
AC AAF87822;
XX
PT 11-JUL-2001 (first entry)
XX
DB Human haemopoietin receptor protein NR12.5 encoding cDNA SEQ ID NO:9.
XX
KM Human; haemopoietin receptor protein; NR12; immunosuppressive;
XX anti-allergic; haemopoietin factor; autoimmune disease; tissue rejection;
XX metal allergy; pollen allergy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1890
FT FT /*tag= a
FT FT /product= "NR12.5"
FT FT /note= "haemopoietin receptor protein"
XX
PN MO200123556-A1.
XX
PD 05-APR-2001.
XX
PF 27-SEP-2000; 2000MO-JP006654.
XX
PR 27-SEP-1999; 99JP-00273358.
XX PR 03-AUG-2000; 2000JP-00240397.
XX
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI Maeda M, Yaguchi N;
XX
DR WPI; 2001-26154/27.
XX
DR P-PDB; AAB74967.
XX
PT New hemopoietin receptor protein NR12 useful for screening for new
XX binding factors for potential treatment of autoimmune disease, tissue
XX rejection and allergies.
XX
PS Claim 1; Fig 13; 140pp; Japanese.
XX
CC The present sequence encodes a human haemopoietin receptor protein NR12
XX designated NR12.5. NR12 has immunosuppressive and anti-allergic

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CC activities. NR12 can be used for searching for haemopoietin factors with  
CC the potential for controlling autoimmune disease, (false rejection and  
CC allergies against e.g. metals and pollen  
XX

Sequence 1910 BP; 654 A; 379 C; 352 G; 525 T; 0 U; 0 Other;

Query Match 66.7%; Score 1906; DB 5; Length 1910;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1906; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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QY 119 ATGATATCACTGCTATTCATATGAGATGCAATATAGCCCTTACATCTCTCACTGG 178
DB 1 ATGATATCACTGCTATTCATATGAGATGCAATATAGCCCTTACATCTCTCACTGG 60
QY 179 TGTGATGAGGATTTCAATATATATATGCTGCGCATCTGGGATGAGAACAGCCACA 238
DB 61 TGTGATGAGGATTTCAATATATATATATGCTGCGCATCTGGGATGAGAACAGCCACA 120
QY 239 ATTTTAAATGGGATATGATATCTATATATTTGCCAAGCAGCAATTAAGAATGCA 298
DB 121 ATTTTAAATGGGATATGATATCTATATATTTGCCAAGCAGCAATTAAGAATGCA 180
QY 299 CCAAGGAACTTCATTTTATATATATGATGATCAAGAAAGATTTCAATCACAAGAT 358
DB 181 CCAAGGAACTTCATTTTATATATATATGATGATCAAGAAAGATTTCAATCACAAGAT 240
QY 359 AATATATCAACAGCTGCTGCTTTGATATATATTTCTGGAACCAATGCTTTATATG 418
DB 241 AATATATCAACAGCTGCTGCTTTGATATATATTTCTGGAACCAATGCTTTATATG 300
QY 419 TGCATGCTGATATGCTCCAAACATTTTCAAGAGACAATGATGATGAGAAAGATTTCT 478
DB 301 TGCATGCTGATATGCTCCAAACATTTTCAAGAGACAATGATGATGAGAAAGATTTCT 360
QY 479 TCTGATATCTCCGAGATATCTGATATGATATCTGATATGATATATGATATGATG 538
DB 361 TCTGATATCTCCGAGATATCTGATATGATATCTGATATGATATATGATATGATG 420
QY 539 AACATATCTTGCACCTGGAATGCTTGGAGATCTCACTTATATATATATATATATG 598
DB 421 AACATATCTTGCACCTGGAATGCTTGGAGATCTCACTTATATATATATATATG 480
QY 599 CATGTAAGAGATTTTGAAGACAGAAAGACACATATCTCACTCAAGCTATATATTA 658
DB 481 CATGTAAGAGATTTTGAAGACAGAAAGACACATATCTCACTCAAGCTATATATTA 540
QY 659 ATCTCAGCTGATTCATTAACAAGGTGCAAGATCTTGGTTTGGTCCAGCAGCAAA 718
DB 541 ATCTCAGCTGATTCATTAACAAGGTGCAAGATCTTGGTTTGGTCCAGCAGCAAA 600
QY 719 GCACTAGGACATGGAAGATCAAAACATGCAAAATTCACCTGATATATATATATAT 778
DB 601 GCACTAGGACATGGAAGATCAAAACATGCAAAATTCACCTGATATATATATATAT 660
QY 779 TCTGAGCCGCTATTTCCAGGAGCTGAGACTATATATGCTACAGTGCACCAATAT 838
DB 661 TCTGAGCCGCTATTTCCAGGAGCTGAGACTATATATGCTACAGTGCACCAATAT 720
QY 839 TATTTGGATAGTCAAAACAATTTGAAGAGTTTCTGATGAAATGATATCAAGGCT 898
DB 721 TATTTGGATAGTCAAAACAATTTGAAGAGTTTCTGATGAAATGATATCAAGGCT 780
QY 899 ACAAAACCAACTTGAATGTTAAAGATTTGACACCAATTTTATATATGCTCAACG 958
DB 781 ACAAAACCAACTTGAATGTTAAAGATTTGACACCAATTTTATATATGCTCAACG 840
QY 959 GAATTTCTAGTGAAGCAAAACATTTAAGTACGATTTCAAGTGAATGCTCAAGAAC 1018
DB 841 GAATTTCTAGTGAAGCAAAACATTTAAGTACGATTTCAAGTGAATGCTCAAGAAC 900
QY 1019 AAAAGTACTGAGCCTTGGAGTCAACGTTTTCATTAACACCTGAAACAGTTCC 1078
DB 901 AAAAGTACTGAGCCTTGGAGTCAACGTTTTCATTAACACCTGAAACAGTTCC 960
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QY 1079 CAGGTACATCAAAAGCATTTCCAAATGACACATGGAATTTGGGCTAACAGTTGCTCC 1138
DB 961 CAGGTACATCAAAAGCATTTCCAAATGACACATGGAATTTGGGCTAACAGTTGCTCC 1020
QY 1139 ATCTTCAAGGAGCCTTACTTCTGACAAACAGAGAGACATTTGATTTATGGGATG 1198
DB 1021 ATCTTCAAGGAGCCTTACTTCTGACAAACAGAGAGACATTTGATTTATGGGATG 1080
QY 1199 ATGCTCTTGGCTATATGTTGATATCTTTCTTTGATTTGGATATTTAACAATCTTC 1258
DB 1081 ATGCTCTTGGCTATATGTTGATATCTTTCTTTGATTTGGATATTTAACAATCTTC 1140
QY 1259 CGAAGTGGATTTAAAGAGATCTTATGTTATATCAAGAGGCTTTATGAAGATAT 1318
DB 1141 CGAAGTGGATTTAAAGAGATCTTATGTTATATCAAGAGGCTTTATGAAGATAT 1200
QY 1319 CCTATATGAAAAACAGCAATGTTGTAAATGCTA CAGGAAAAATGTAACCTTATGAAT 1378
DB 1201 CCTATATGAAAAACAGCAATGTTGTAAATGCTA CAGGAAAAATGTAACCTTATGAAT 1260
QY 1379 AATATTTCCAGTGAAGAGCTCTATATGTTGATCCCATGATTCAGAGATTAAGAAATC 1438
DB 1261 AATATTTCCAGTGAAGAGCTCTATATGTTGATCCCATGATTCAGAGATTAAGAAATC 1320
QY 1439 TTCAATCCAGAAACAGAGGCTACAGCTA CAGGAGAGAAATACAGGACCCCTGAGACA 1498
DB 1321 TTCAATCCAGAAACAGAGGCTACAGCTA CAGGAGAGAAATACAGGACCCCTGAGACA 1380
QY 1499 AGAGACTACCCGAAACCTCGCTATTCGCAATATCTACAGTTGATATATATCTCTGATCTC 1558
DB 1381 AGAGACTACCCGAAACCTCGCTATTCGCAATATCTACAGTTGATATATATCTCTGATCTC 1440
QY 1559 AACCTGATATTAACCCCAATTTTCAATTTTCTGCTGAGGAAACCATCTCAGCAAT 1618
DB 1441 AACCTGATATTAACCCCAATTTTCAATTTTCTGCTGAGGAAACCATCTCAGCAAT 1500
QY 1619 AATATGAATATATCTTCTTAACTTAACTTAAACCAAGGATGATCTTAACTGAGAAAT 1678
DB 1501 AATATGAATATATCTTCTTAACTTAACTTAAACCAAGGATGATCTTAACTGAGAAAT 1560
QY 1679 AATCCAGGTTACAAAGCATCTTAAATTTTCTTTTCTGTTTCAAGTGAATTCAT 1738
DB 1561 AATCCAGGTTACAAAGCATCTTAAATTTTCTTTTCTGTTTCAAGTGAATTCAT 1620
QY 1739 AGCAACAATATTTCTTGAAGATTAAGCTCTATATTAATCAAGAGATTCAGTTCT 1798
DB 1621 AGCAACAATATTTCTTGAAGATTAAGCTCTATATTAATCAAGAGATTCAGTTCT 1680
QY 1799 CCTGACATCAAAACCTGATGAGGAGAAACCAACATCTTTTGAAGAAATGATCAACC 1858
DB 1681 CCTGACATCAAAACCTGATGAGGAGAAACCAACATCTTTTGAAGAAATGATCAACC 1740
QY 1859 AGTGAACATATTTCCAGAACAGACCCCTGCTCTGATGAATTTCTCTGTTTGGGATC 1918
DB 1741 AGTGAACATATTTCCAGAACAGACCCCTGCTCTGATGAATTTCTCTGTTTGGGATC 1800
QY 1979 TTCAATAGATTTCACTCTTGAAGAAATGAGCTGTTGCTCAAAATCA 2028
DB 1861 TTCAATAGATTTCACTCTTGAAGAAATGAGCTGTTGCTCAAAATCA 1910
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RESULT 7  
ADV43392  
ID ADV43392 standard; cDNA; 1890 BP.  
XX  
AC ADV43392;  
XX  
XX  
DT 10-MAR-2005 (first entry)

XX Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 1020.  
 DE microarray; psychoneuroendocrinimmune; chronic fatigue;  
 XX non-insulin dependent diabetes; allergy; immune disorder; inflammation;  
 KM cancer; neoplasm; infection; expressed sequence tag; ss.  
 XX  
 OS Homo sapiens.  
 PN M02004108899-A2.  
 XX  
 PD 16-DEC-2004.  
 XX  
 PF 04-JUN-2004; 2004MO-US017686.  
 XX  
 PR 04-JUN-2003; 2003US-0475915P.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Nicholson A, Vernon SD;  
 DR WPI; 2005-031682/03.  
 XX  
 PS Claim 1; SEQ ID NO 1020; 254bp; English.  
 XX  
 CC The invention relates to a new microarray which comprises probes for  
 CC genes involved in psychoneuroendocrinimmune (PNI) activity. The  
 CC microarray is useful in diagnosing a condition associated with PNI  
 CC activity, such as CFS, type-2 diabetes, allergic condition, inflammation,  
 CC cancer and infection. The present sequence represents a  
 CC psychoneuroendocrinimmune gene expressed sequence tag. Note the  
 CC specificatio mentions SEQ ID NO of up to 3314 but only sequences up to  
 CC SEQ ID NO 1829 are provided.  
 XX  
 SQ Sequence 1890 BP; 647 A; 377 C; 347 G; 519 T; 0 U; 0 Other;

Query Match 66.1%; Score 1887.6; DB 14; Length 1890;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1887; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 119 ATGAATCAAGTCACTATTCAATGAGATGAGTAAAGCCCTTACATCTCAAGCTGG 178  
 DB 1 ATGAATCAAGTCACTATTCAATGAGATGAGTAAAGCCCTTACATCTCAAGCTGG 60

QY 179 TGTGATGAGGAATTA CAATATATAACTGCTGGCCACATCTGGGTAGAACCAGCCACA 238  
 DB 61 TGTGATGAGGAATTA CAATATATAACTGCTGGCCACATCTGGGTAGAACCAGCCACA 120

QY 239 ATTTTAAAGATGGGTATGAAATATCTATATATTTGCCAAGCAATTAAGAACTGCCAA 238  
 DB 121 ATTTTAAAGATGGGTATGAAATATCTATATATTTGCCAAGCAATTAAGAACTGCCAA 180

QY 299 CCAAGGAACTTATTTTATTAATAAATGCGATCAAGAAAGATTTCATATCAAGGATT 358  
 DB 181 CCAAGGAACTTATTTTATTAATAAATGCGATCAAGAAAGATTTCATATCAAGGATT 240

QY 359 AATTAACAACAGAGCTGGCTTTGGTATTAATAAATCTTTCTGGAACCAATGCTTATGTAC 418  
 DB 241 AATTAACAACAGAGCTGGCTTTGGTATTAATAAATCTTTCTGGAACCAATGCTTATGTAC 300

QY 419 TGGACGTGGAATGTCCTCAACATTTTCAAGAGACCTGATATGTGAAAAGCAATTTCT 478  
 DB 301 TGGACGTGGAATGTCCTCAACATTTTCAAGAGACCTGATATGTGAAAAGCAATTTCT 360

QY 479 TCGGATATCGGCAAGATATTTCTGATGAAGTAACTGTCTCAATTAATGAAATTCAGGC 538  
 DB 361 TCGGATATCGGCAAGATATTTCTGATGAAGTAACTGTCTCAATTAATGAAATTCAGGC 420

QY 539 AACATGACTTGCACCTGGAAATGCTGGAAAGCTCACTACATATAGACCAAAATACGTGTA 598  
 DB 421 AACATGACTTGCACCTGGAAATGCTGGAAAGCTCACTACATATAGACCAAAATACGTGTA 480

QY 599 CATTGGAAGGTTTAAAGACAGAAAGAGCAACAGTATCTCACTCAAGCTATATTAAC 658  
 DB 481 CATTGGAAGGTTTAAAGACAGAAAGAGCAACAGTATCTCACTCAAGCTATATTAAC 540

QY 659 ATCTCCACTGATTCATTACAAAGGTGCAAGAAATCTTGGTTGGTCCAAAGCAAGCAAC 718  
 DB 541 ATCTCCACTGATTCATTACAAAGGTGCAAGAAATCTTGGTTGGTCCAAAGCAAGCAAC 600

QY 719 GCACTAGGCAATGGAAGATGCAAAACATGCAAAATTCACCTGGATATATAGTAACTCT 778  
 DB 601 GCACTAGGCAATGGAAGATGCAAAACATGCAAAATTCACCTGGATATATAGTAACTCT 660

QY 779 TCTGACCGGTCAATTTCCAGGGCTGAGACTAATTAATGCTACAGTGGCCAAAGACATTAAT 838  
 DB 661 TCTGACCGGTCAATTTCCAGGGCTGAGACTAATTAATGCTACAGTGGCCAAAGACATTAAT 720

QY 839 TATTGGATAGTCAAAACAAATTGAAAAGTTTCTGTGAATGAATPAAAGCTTACA 898  
 DB 721 TATTGGATAGTCAAAACAAATTGAAAAGTTTCTGTGAATGAATPAAAGCTTACA 780

QY 899 ACAAACCAACTTGGAAATGTTAAAGATTTGACACCAATTTTACATATGTCGAACAGTCA 958  
 DB 781 ACAAACCAACTTGGAAATGTTAAAGATTTGACACCAATTTTACATATGTCGAACAGTCA 840

QY 959 GAATTTACTTGGAGGCCAAACATTAAGTACGTATTTCAAGTACAGTGTCAAGAACAGGC 1018  
 DB 841 GAATTTACTTGGAGGCCAAACATTAAGTACGTATTTCAAGTACAGTGTCAAGAACAGGC 900

QY 1019 AAAAGTACTGAGAGCTTGGAGTTGACCGTTTTCATPAAACACCTGAACAGTTCCC 1078  
 DB 901 AAAAGTACTGAGAGCTTGGAGTTGACCGTTTTCATPAAACACCTGAACAGTTCCC 960

QY 1079 CAGGTACATCAAAAGACATTCACACATGACATGGAATTTGGGGCTAACAGTTGCTTC 1138  
 DB 961 CAGGTACATCAAAAGACATTCACACATGACATGGAATTTGGGGCTAACAGTTGCTTC 1020

QY 1139 ATCTTACAGGGGACCTTACTTCTGACACAGAGAGACATTTGATTTTGGGAATG 1198  
 DB 1021 ATCTTACAGGGGACCTTACTTCTGACACAGAGAGACATTTGATTTTGGGAATG 1080

QY 1199 ATCGTCTTGGCTGTTATGTTGTCATCTTTCTTTGATTTGGATATTTAACAGATCATTC 1258  
 DB 1081 ATCGTCTTGGCTGTTATGTTGTCATCTTTCTTTGATTTGGATATTTAACAGATCATTC 1140

QY 1259 CGAAGTGGATTTAAAGAAAGATCTTAATGTTTAATCCAAAGTGGCTTTATGAAAGATTT 1318  
 DB 1141 CGAAGTGGATTTAAAGAAAGATCTTAATGTTTAATCCAAAGTGGCTTTATGAAAGATTT 1200

QY 1319 CCTAATATGAAAAACAGCAATGTTGTAATGCTACAGAAATTTAGTAACTTATGAAT 1378  
 DB 1201 CCTAATATGAAAAACAGCAATGTTGTAATGCTACAGAAATTTAGTAACTTATGAAT 1260

QY 1379 AATTAATTCAGTGAAGAGGTCTTAATGTTGATGCCATGATTAACAGAGATTAAGAAATC 1438  
 DB 1261 AATTAATTCAGTGAAGAGGTCTTAATGTTGATGCCATGATTAACAGAGATTAAGAAATC 1320

QY 1439 TTGATCCCAAGAACACAAAGCTTACAGACTACAGAAAGAAATACAGAACCCCTGGAGACA 1498  
 DB 1321 TTGATCCCAAGAACACAAAGCTTACAGACTACAGAAAGAAATACAGAACCCCTGGAGACA 1380

QY 1499 AGAGACTACCCGCAAAATCGCTATTCGACAAATACAGTGTATATATTCCTGATCTC 1558  
 DB 1381 AGAGACTACCCGCAAAATCGCTATTCGACAAATACAGTGTATATATTCCTGATCTC 1440

QY 1559 AACACTGATATTAACCCCAATTTCAAAATTTTCTGCTGAGGGAAGCACTCAGCAAT 1618  
 DB 1441 AACACTGATATTAACCCCAATTTCAAAATTTTCTGCTGAGGGAAGCACTCAGCAAT 1500

QY 1619 AATTAAGAAATTAATCTTCACTTAACACTTAACCAACAGTTGATTCCTTAAGCTCAGGAAT 1678

Db	1501	AAATATGAAATTA	CTCTCTTAACCTTA	ACAACCAAGTTGA	ATCTCTTAAGCTCAGAA	AAAT	1560
Qy	1679	AATCCCAAGTTACA	AAAAGCATCTAA	ATTTTCTTTTCTGT	TTCAGAGTGAATTC	ACTA	1738
Db	1561	AATCCCAAGTTACA	AAAAGCATCTTA	TTTGTCTTTTCTGT	TTCAGAGTGAATTC	ACTA	1620
Qy	1739	AGCAACACAATAT	TTTCTTTGGAGAA	TTAAGCTCATAT	TAAATCAAGAAATG	CAGTTCT	1798
Db	1621	AGCAACACAATAT	TTTCTTTGGAGAA	TTAAGCTCATAT	TAAATCAAGAAATG	CAGTTCT	1680
Qy	1799	CCTGACATACAAA	CTCAGTAGAGAG	AGAAACAACATG	CTTTTGGAAAATG	ATTCACCC	1858
Db	1681	CCTGACATACAAA	CTCAGTAGAGAG	AGAAACAACATG	CTTTTGGAAAATG	ATTCACCC	1740
Qy	1859	AGTGAATCTATTC	AGAAACAAGCCT	CTCTTCTCTGA	TGAATTTGTCTCT	GTTTGGGATC	1918
Db	1741	AGTGAATCTATTC	AGAAACAAGCCT	CTCTTCTCTGA	TGAATTTGTCTCT	GTTTGGGATC	1800
Qy	1919	GTCGATGAGGAG	TGGCCATCTAT	TAAATCTATTTT	CCACAAAATATTT	TGGAAAGCCAC	1978
Db	1801	GTCGATGAGGAG	TGGCCATCTAT	TAAATCTATTTT	CCACAAAATATTT	TGGAAAGCCAC	1860
Qy	1979	TTCAATAGGATTT	CACTCTGGAAAA	AGTAG	2008		
Db	1861	TTCAATAGGATTT	CACTCTGGAAAA	AGTAG	1890		

RESULT 8  
AAD38774  
ID AAD38774 standard; DNA; 1698 BP.

DT 23-SEP-2002 (first entry)

DE Human haematopoietin receptor 2 (HPR2) ex8-ex9 DNA.

KM Human, haemotopoietin receptor; receptor; HRR1, HPR2; cell proliferation,  
 KM pancytopenia; leukopenia; anaemia; thrombocytopaenia; osteoporosis;  
 KM neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder;  
 KM cancer; myeloid myelastomatous syndrome; idiopathic thrombocytopenic purpura;  
 KM ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;  
 KM osteoclast disorder; periodontitis; acute polynuropathy; Bell's palsy;  
 KM amyotonia nervosa; chronic fatigue syndrome; Creutzfeldt-Jacob disease;  
 KM demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;  
 KM vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;  
 KM stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;  
 KM ischaemic disease; gene; ds.

**OS Homo sapiens.**

FH	Key	Location/Qualifiers

FT / \*tag= a

XX:

PD 11-APR-2002.

PF 05-OCT-2001; 2001WO-US031634.

PR 06-OCT-2000; 2000US-0238706P.

PR 20-FEB-2001; 2001US-0270282P.

PA (IMMV ) IMMUNEX CORP.

PI Cosman DJ. Mosley BA. Bird TA. Dubose RF. Wiley SR.

WPI: 2002-330172/36.

DR P-PSDB; AAE24034.

XX Human and murine hematopoietin receptor polypeptides HPR1 and HPR2,  
PT useful for treating cell proliferation, metabolic, and reproductive  
PT hormone related conditions.  
XX  
PS Claim 9, Page 123-124, 136pp; English.

Claim 9; Page 123-124; 136pp; English.

The present invention relates to human and murine haematopoietic receptor polypeptides HPR1 and HPR2. Sequences of the invention are useful for treating cell proliferation conditions e.g., pancytopenia, leukopenia, anaemia, thrombocytopaenia, neurodegenerative disorders and osteoporosis resulting from a lack of bone-forming cells. They are also useful for treating cell proliferation conditions such as leukaemia and tumour metastasis, osteoporosis resulting from an excess of bone-resorbing cells. HPR sequences are also useful for treating medical conditions and diseases such as cell proliferation, metabolic and reproductive hormone related conditions. They are useful for treating various haematological and oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell, cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma, sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer), squamous cell carcinoma), haematologic disorders, anaemias (e.g., anaemia of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelodysplastic syndromes (including refractory anaemia, refractory anaemia with ringed sideroblasts or with excess blasts), idiopathic thrombocytopenic purpura (ITP), sickle cell vasoocclusive crisis, myelofibrosis/myeloid metaplasia, osteoclast disorders that lead to bone loss such as osteoporosis including post-menopausal osteoporosis, periodontitis resulting in tooth loosening or loss, prosthesis loosening after joint replacement, neurodegenerative conditions (e.g., acute polyneuropathy, Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible dementia including Creutzfeldt-Jacob disease, dementiating neuropathy, Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome, myasthenia gravis, chronic neuronal degeneration, stroke including cerebral ischaemic diseases. HPR1 and HPR2 polypeptides are also useful for treating various other disorders such as osteoporosis, obesity, deficient mammary development and infertility. The present sequence is human HPR2 ex8-ex9 DNA

Sequence 1698 BP; 597 A; 335 C; 310 G; 456 T; 0 U; 0 Other;

Query Match 52.3%; Score 1493.6; DB 6; Length 1698;

Matches 1695; Conservative 2; Mismatches 1; Indels 192; Gaps 1;

119 ATGATCAKGTCACTATTCAATGGATGCAGTATAGCCCTTACATACTCTCAGCTGG 178

Db 1 ATGAATCAGGCTACTATTCAATGGGATGCAGTATAGCCCTTACATACTCTTCAGCTGG 60

179 TGTTCATGGAGGAATTACAAATATAAACTGCTCTGGCCACATCTGGTAGAACCAAGCCACA 238

61 TGTCA TGGAGGAA TTTACA AATATA AACTG CTCTGG CCACTCT GGTAG AACCAC CACA 120

239 ATTTTAAAGATGCGTATGAATATCTCTATATATTGCCAAGCAGCAATTAAGAACCTGCCAA 298

121 ATTTTATACATGCTATGAAATATCTCTTATATATTGCTCAAGCAGCAATTAAAGCACTGCCA 180

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QY 539 AACATGACTTGCACCTGGAATGCTGGAACTCACTACATAGACAAATACTGTGTA 598  
 DB 421 AACATGACTTGCACCTGGAATGCTGGAACTCACTACATAGACAAATACTGTGTA 480  
 QY 599 CATGTGAAGATTAGAGACAGAAAGAGCAACAGTATCTCACCTCAGCTATATTAC 658  
 DB 481 CATGTGAAGATTAGAGACAGAAAGAGCAACAGTATCTCACCTCAGCTATATTAC 540  
 QY 659 ATCTCCAGTATTCATTACAAAGGTGGCAGAGAGTATCTGTGGGTCCAAAGCAGAAC 718  
 DB 541 ATCTCCAGTATTCATTACAAAGGTGGCAGAGAGTATCTGTGGGTCCAAAGCAGAAC 600  
 QY 719 GCACTAGGACATGAGAGAGTCAAAACCACTGCAATTCACCTGAGATGATAGTATCT 778  
 DB 601 GCACTAGGACATGAGAGAGTCAAAACCACTGCAATTCACCTGAGATGATAGTATCT 660  
 QY 779 TCTGCAAGCCGTCTATTCAGGGCTGAGACTATTAATGCTACAGTCCCAAGACATATT 838  
 DB 661 TCTGCAAGCCGTCTATTCAGGGCTGAGACTATTAATGCTACAGTCCCAAGACATATT 720  
 QY 839 TATTGGGATAGTCAACCAATTTGAAGAGTTTCTGTGAAATGAGATCAAGGCTACA 898  
 DB 721 TATTGGGATAGTCAACCAATTTGAAGAGTTTCTGTGAAATGAGATCAAGGCTACA 780  
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 DB 841 GAATTTCTACTGAGCCAACTTAAGTACGATATTTCAAGTGAGATGTCAGAAACAGGC 900  
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 DB 901 AAAAGGATCTGGAGCCTTGGAGTCAACGTTTTTTCATATAACACTGAAACAGTTCCC 954  
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 DB 955 ----- 954  
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 DB 955 ----- 954  
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 DB 955 ----- 954  
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 QY 1739 AGCAACACATATTTCTGAGAGATTAAGCTCATATTAATCAAGAGATGCAATTC 1798  
 DB 1429 AGCAACACATATTTCTGAGAGATTAAGCTCATATTAATCAAGAGATGCAATTC 1488  
 QY 1799 CTTGACATACAAACCTCAGTAGAGAGAAACCACTGCTTTTGGAAAAATGATCACCC 1858  
 DB 1489 CTTGACATACAAACCTCAGTAGAGAGAAACCACTGCTTTTGGAAAAATGATCACCC 1548  
 QY 1859 AGTGAATCTATTCAGAACAGACCCCTGCTCGATGAATTTGTCTGTTTGGGGAATC 1918  
 DB 1549 AGTGAATCTATTCAGAACAGACCCCTGCTCGATGAATTTGTCTGTTTGGGGAATC 1608  
 QY 1919 GTGAATGAGAGATTCGATCTATTAATTAATTTTCCAAATAATTTTGGAAACCCAC 1978  
 DB 1609 GTGAATGAGAGATTCGATCTATTAATTAATTTTCCAAATAATTTTGGAAACCCAC 1668  
 QY 1979 TTCAATAGATTTCACTCTTGGAAAAATG 2008  
 DB 1669 TTCAATAGATTTCACTCTTGGAAAAATG 1698

RESULT 9  
 AAK98258  
 ID AAK98258 standard; DNA; 1887 BP.  
 XX  
 AC AAK98258;  
 DT 28-MAY-2002 (first entry)  
 XX  
 DE Human DNAX cytokine receptor subunit 5 (DCR5) reverse translation DNA.  
 XX  
 KM Human: DNAX cytokine receptor subunit 5; DCR5; IL30 receptor;  
 KM immune response; DCR5; p40/IL-30 ligand; cell physiology modulation;  
 KM cell development modulation; TH1-mediated disease; multiple sclerosis;  
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KM diabetes; psoriasis; sepsis; allogeneic transplant; recipient;  
 KM TH2 response; tumour; viral growth; fungal growth; vaccine;  
 KM allergic response; ss; reverse translation.  
 XX  
 OS Homo sapiens.  
 XX  
 PN NC0200185790-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 10-MAY-2001; 2001MO-US015057.  
 XX  
 PR 10-MAY-2000; 2000US-0203426P.  
 XX  
 PA (SCHE ) SCHERING CORP.  
 XX  
 PI Chirica M, Kastelein RA, Moore KM, Parham CL;  
 XX  
 DR WPI; 2002-062238/08.  
 XX  
 PT Novel DNAX cytokine receptor subunit 5 polypeptide which is subunit of  
 PT receptor complex for p40/IL-30, useful for treating conditions  
 PT associated with abnormal expression or triggering of response to p40/IL-  
 PT B30 ligand.  
 XX  
 PS Disclosure; Page 13; 74pp; English.  
 XX  
 CC The present DNA sequence represents a reverse translation of the human  
 CC DNAX cytokine receptor subunit 5 (defined as DCR5 or IL30 receptor) of  
 CC the invention. DCR5 is a member of the class I branch of the cytokine

receptor superfamily and is closely related to the IL-6 receptor subunit gp130 and the IL-12R-beta-2 subunit. Cytokines are soluble molecules which play a critical role in controlling the complex cellular interactions of the immune response. The invention comprises novel receptors related to cytokine receptors designated DNAX cytokine receptor subunits (DCRS). Specifically the invention comprises a subunit (DCRS5) for a receptor complex for the p40/IL-30 ligand. The DCRS5 proteins of the invention are useful for treating diseases or disorders associated with abnormal expression or abnormal triggering of response to the p40/IL-30 ligand. The proteins of the invention can be used to modulate the physiology or development of a cell from a host which exhibits TH- mediated disease; multiple sclerosis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; diabetes; psoriasis; sepsis; an allogeneic transplant recipient; chronic TH2 response; tumour; viral or fungal growth; vaccine recipient; or an allergic response

Sequence 1887 BP; 421 A; 183 C; 245 G; 257 T; 0 U; 781 Other;

Query Match 48.3%; Score 1379; DB 6; Length 1887;

Best Local Similarity 58.6%; Pred. No. 0;

Matches 1106; Conservative 491; Mismatches 290; Indels 0; Gaps 0;

119 ATGAATCACTCACTATTCATGAGATGCAAGTAATAGCCCTTACATATCTTCAGCTGG 178  
1 ATGAATCACTCACTATTCATGAGATGCAAGTAATAGCCCTTACATATCTTCAGCTGG 60  
179 TGTCAATGAGAGATTCATTAATATTAATGCTCTGGCCCAATCTGGGTAGAACCCAGCCACA 238  
61 TGTCAATGAGAGATTCATTAATATTAATGCTCTGGCCCAATCTGGGTAGAACCCAGCCACA 120  
239 ATTTTAAAGATGGATGATATCTCTATATATTCAGCAAGCAAGATTAAGATTCGCA 298  
121 ATTTTAAAGATGGATGATATCTCTATATATTCAGCAAGCAAGATTAAGATTCGCA 180  
299 CCAAGGAATCTTCAATTTTAAATATGATGCAAGCAAGATTTCAATCAAGGAT 358  
181 CCAAGGAATCTTCAATTTTAAATATGATGCAAGCAAGATTTCAATCAAGGAT 240  
359 AATTAATCAACACCTGCTGGCTTGTATTAATACTTCTGGAACCAATGCTTCTATGCTAC 418  
241 AATTAATCAACACCTGCTGGCTTGTATTAATACTTCTGGAACCAATGCTTCTATGCTAC 300  
419 TGCATGCTGAATGCTCCCAACATTTTCAAGACAGACATGATATGGAAGAAACATTTCT 478  
301 TGCATGCTGAATGCTCCCAACATTTTCAAGACAGACATGATATGGAAGAAACATTTCT 360  
479 TGTGAATATCCGCGCAATATTTCTGATGAAGTAACCTGTCTATTAATATGATATTCAGGC 538  
361 TGTGAATATCCGCGCAATATTTCTGATGAAGTAACCTGTCTATTAATATGATATTCAGGC 420  
539 AATCATGATCTGCACCTGGAATGCTGGAAGCTCACTACATACACAAATATAGTGTGA 598  
421 AATCATGATCTGCACCTGGAATGCTGGAAGCTCACTACATACACAAATATAGTGTGA 480  
599 CATGTGAGAGATTTAGAGACAGAAAGACATGATATCTCACTCACTCACTATTAATCA 658  
481 CATGTGAGAGATTTAGAGACAGAAAGACATGATATCTCACTCACTCACTATTAATCA 540  
659 ATCTCCACTGATTCATTAACAAGGTGCGAAGAGTACTGTTGGTCCAAGCAGCAAC 718  
541 ATCTCCACTGATTCATTAACAAGGTGCGAAGAGTACTGTTGGTCCAAGCAGCAAC 600  
719 GCACTAGGATGGAAGAGTCAAAAACATGCAATTCCTGATGATATATAGTATCTCT 778  
601 GCACTAGGATGGAAGAGTCAAAAACATGCAATTCCTGATGATATATAGTATCTCT 660  
779 TGTGAGAGCTGATTCAGAGCTGAGATTAATATCTCACTCACTCACTATTAATCA 838  
661 TGTGAGAGCTGATTCAGAGCTGAGATTAATATCTCACTCACTCACTATTAATCA 720  
839 TATTTGGATAGTCAAAACATTAATGAAGATTTCTGTAATATGAGATTAAGGCTTACA 898  
721 TATTTGGATAGTCAAAACATTAATGAAGATTTCTGTAATATGAGATTAAGGCTTACA 780

899 ACAACCAACTGATGATTTAAAGATTTGACACCAATTTTACATATGTCACACACTCA 958  
781 ACNAATCAACATGATGATTTAAAGATTTGACACCAATTTTACATATGTCACACACTCA 840  
959 GAATTTACTTGGAGCCAAACATTAAGTACGATATTTCAAGTACATGATGTCACACAGC 1018  
841 GATTTATATATGATGATTTAAAGATTTGACACCAATTTTACATATGTCACACACTCA 900  
1019 AAAAGTACCTGAGCTTGGATTTGACACCAATTTTACATATGTCACACACTCA 1078  
901 AAAAGTACCTGAGCTTGGATTTGACACCAATTTTACATATGTCACACACTCA 960  
1079 CAGTGCATCAAAAGATTTCAACATGACATGATGATTTGAGGCTTCAAGTGTCTTC 1138  
961 CAGTGCATCAAAAGATTTCAACATGACATGATGATTTGAGGCTTCAAGTGTCTTC 1020  
1139 ATCTTCAAGGAGCCTTACTTCTGACACACAGAGACATTTGATTTATGGAATG 1198  
1021 ATCTTCAAGGAGCCTTACTTCTGACACACAGAGACATTTGATTTATGGAATG 1080  
1199 ATCTTCTGCTGATATGTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 1258  
1081 ATCTTCTGCTGATATGTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 1240  
1259 CGAATGAGGATTTAAAGAGATTTATGTTAATACCAAGGATTTGATTTGATTTG 1318  
1141 CGAATGAGGATTTAAAGAGATTTATGTTAATACCAAGGATTTGATTTGATTTG 1280  
1319 CCTAATATGAAAAACAGCAATGTTGTAATGCTACAGGAAAAATGATGATTTATG 1378  
1201 CCTAATATGAAAAACAGCAATGTTGTAATGCTACAGGAAAAATGATGATTTATG 1260  
1379 AATTAATCAACACCTGCTGGCTTGTATTAATACTTCTGGAACCAATGCTTCTATGCTAC 1438  
1261 AATTAATCAACACCTGCTGGCTTGTATTAATACTTCTGGAACCAATGCTTCTATGCTAC 1320  
1439 TGCATGCTGAATGCTCCCAACATTTTCAAGACAGACATGATATGGAAGAAACATTTCT 1498  
1321 TGCATGCTGAATGCTCCCAACATTTTCAAGACAGACATGATATGGAAGAAACATTTCT 1380  
1499 AGAAGTACCCGCAACATTTCTGATGAAGTAACCTGTCTATTAATATGATATTCAGGC 1558  
1381 AGAAGTACCCGCAACATTTCTGATGAAGTAACCTGTCTATTAATATGATATTCAGGC 1440  
1559 AATCATGATCTGCACCTGGAATGCTGGAAGCTCACTACATACACAAATATAGTGTGA 1618  
1441 AATCATGATCTGCACCTGGAATGCTGGAAGCTCACTACATACACAAATATAGTGTGA 1500  
1619 AATTAATGAATTTACTTCTGATGAAGTAACCTGTCTATTAATATGATATTCAGGC 1678  
1501 AATTAATGAATTTACTTCTGATGAAGTAACCTGTCTATTAATATGATATTCAGGC 1560  
1679 AATCCAGGATTTCAAAAGATTTCTGATGAAGTAACCTGTCTATTAATATGATATTCAG 1738  
1561 AATCCAGGATTTCAAAAGATTTCTGATGAAGTAACCTGTCTATTAATATGATATTCAG 1620  
1739 AGCAACATATATTTCTGGAAGATTTAGCTCATTTAATCAAGAGATGCAATGCTCT 1798  
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1799 CCGTACATCAAAAGCTCAGTACGAGGAGAAACACACATGCTTTTGGAAAAATGATTCACC 1858  
1681 CCGTACATCAAAAGCTCAGTACGAGGAGAAACACACATGCTTTTGGAAAAATGATTCACC 1740  
1859 AGTGAACCTATTTCAAGACAGACCTGCTCTGATGAATTTGCTCTGTTTGGGATC 1918  
1741 AGTGAACCTATTTCAAGACAGACCTGCTCTGATGAATTTGCTCTGTTTGGGATC 1800  
1919 GTGAATGAGAGTGGCATCTATTAATATGATTTTCCAAATAATTTTGGAAAGCCAC 1978  
1801 GTGAATGAGAGTGGCATCTATTAATATGATTTTCCAAATAATTTTGGAAAGCCAC 1860



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QY 1979 TTCAATAGATTTCACCTCTTGAAAAG 2005
DB 1861 TTAAATGNAITHMSNTYNTNGAAR 1887

RESULT 10
AAF87819
ID AAF87819 standard; cDNA; 1479 BP.
AC AAF87819;
XX
XX 11-JUL-2001 (first entry)
DT
XX Human haemopoietin receptor protein NR12.2 encoding cDNA SEQ ID NO:3.
DE
XX
XX Human haemopoietin receptor protein; NR12; immunosuppressive;
KM anti-allergic; haemopoietin factor; autoimmune disease; tissue rejection;
KM metal allergy; pollen allergy; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 98..1384
FT CDS /tag= a
FT /product= "NR12.2"
XX /note= "haemopoietin receptor protein"
PN MO200123556-A1.
XX
XX 05-APR-2001.
PD
XX 27-SEP-2000; 2000MO-JP006654.
PF
XX 27-SEP-1999; 99JP-00273358.
PR 03-AUG-2000; 2000JP-00240397.
XX
XX (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX Maeda M, Yaguchi N;
XX WPI; 2001-266154/27.
XX P-PSDB; AAB74964.
XX
XX New hemopoietin receptor protein NR12 useful for screening for new
XX binding factors for potential treatment of autoimmune disease, tissue
XX rejection and allergies.
XX
XX Claim 1; Fig 5; 140pp; Japanese.
XX
XX The present sequence encodes a human haemopoietin receptor protein NR12
XX designated NR12.2. NR12 has immunosuppressive and anti-allergic
XX activities. NR12 can be used for searching for haemopoietin factors with
XX the potential for controlling autoimmune disease, tissue rejection and
XX allergies against e.g. metals and pollen
XX
XX Sequence 1479 BP; 503 A; 292 C; 298 G; 386 T; 0 U; 0 Other;
SQ
Query Match 46.3%; Score 1322.8; DB 5; Length 1479;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1324; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 28 CAGCCACAAAGAGGTGGAGGCTGGCTGTGAAGTGAATTAATGCTTCAAAACAGTTGAA 87
DB 7 CAGCCACAAAGAGGTGGAGGCTGGCTGTGAAGTGAATTAATGCTTCAAAACAGTTGAA 66
QY 88 AGAGGAGAAACAGTCTTTCTGCTTCCAGACATGAATCAGTCACTATTCAATGGATGC 147
DB 67 AGAGGAGAAACAGTCTTTCTGCTTCCAGACATGAATCAGTCACTATTCAATGGATGC 126
QY 148 AGTAAATGACCTTACATCTTCACTGAGTGTGATGAGAGAAATTAACAATTAACCTG 207
DB 127 AGTAAATGACCTTACATCTTCACTGAGTGTGATGAGAGAAATTAACAATTAACCTG 186
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QY 208 CTCGGCCACATCTGGGTGAAACACGCCAACATTTTAAAGATGGATATATCTCTAT 267
DB 187 CTCGGCCACATCTGGGTGAAACACGCCAACATTTTAAAGATGGATATATCTCTAT 246
QY 268 ATATTGGCAAGCAAGCAATTAAGAACTGCCAACAGAACTTCAATTTTATTAATAATGG 327
DB 247 ATATTGGCAAGCAAGCAATTAAGAACTGCCAACAGAACTTCAATTTTATTAATAATGG 306
QY 328 CATCAAGAAAGATTTCAATCCACAAAGATTAATAAACAACAGCTCGCTTGGATTA 387
DB 307 CATCAAGAAAGATTTCAATCCACAAAGATTAATAAACAACAGCTCGCTTGGATTA 366
QY 388 AAACTTTGGAACCAATGCTTTCTATGATCTGACCTGTAATGTCCTCAATTTTCA 447
DB 367 AAACTTTGGAACCAATGCTTTCTATGATCTGACCTGTAATGTCCTCAATTTTCA 426
QY 448 AGAGACATGATATGAGGAAAGAAACATTTCTTGATATCCGCGCATATTCCTGATGA 507
DB 427 AGAGACATGATATGAGGAAAGAAACATTTCTTGATATCCGCGCATATTCCTGATGA 486
QY 508 AGTAACCTGTGATTTATGAATATTTCAAGCAACATGACTTGACCTGGAAATGCTTGAA 567
DB 487 AGTAACCTGTGATTTATGAATATTTCAAGCAACATGACTTGACCTGGAAATGCTTGAA 546
QY 568 GCTCACTTACATGACACAAATACCTGGTACATGTGAAGATTTAGACACAGAAAGA 627
DB 547 GCTCACTTACATGACACAAATACCTGGTACATGTGAAGATTTAGACACAGAAAGA 606
QY 628 GCAACAGTATCTCACTCAAGCTATTTAAATCTTCCATGATCTTCAAGAGTGGCAA 687
DB 607 GCAACAGTATCTCACTCAAGCTATTTAAATCTTCCATGATCTTCAAGAGTGGCAA 666
QY 688 GAAGTACTTGTGTTGGTCCAAAGCAGCAAAACGCACTAGGCAATGAAAGTCAAAACACT 747
DB 667 GAAGTACTTGTGTTGGTCCAAAGCAGCAAAACGCACTAGGCAATGAAAGTCAAAACACT 726
QY 748 GCAATTCACCTGGATGATATAGTATACCTTGTGAGCCGTCATTTCCAGGGCTGAGAC 807
DB 727 GCAATTCACCTGGATGATATAGTATACCTTGTGAGCCGTCATTTCCAGGGCTGAGAC 786
QY 808 TATTAATGCTACAGTGGCCAAAGCAATTTTATGGGATAGTCAACAAATTAAGAAA 867
DB 787 TATTAATGCTACAGTGGCCAAAGCAATTTTATGGGATAGTCAACAAATTAAGAAA 846
QY 868 GGTTCCTGTGAATAGATACAGGCTACAAACAAACCAACTTGAATGTTAAAGATT 927
DB 847 GGTTCCTGTGAATAGATACAGGCTACAAACCAACTTGAATGTTAAAGATT 906
QY 928 TGACACCAATTTTACATATGTGCAACAGTCAGATTTCTATGGAGCCAAACATTAAGTA 987
DB 907 TGACACCAATTTTACATATGTGCAACAGTCAGATTTCTATGGAGCCAAACATTAAGTA 966
QY 988 CGTATTTCAAGTGAATGTCAGAAACAGGCAAAAGATGCTGGACGCTTGGAGTTCAAC 1047
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QY 1048 GTTTTTCATTAACCACTGAAACAGTTCCCGAGTCAATCAAAAGCAATTCACATGA 1107
DB 1027 GTTTTTCATTAACCACTGAAACAGTTCCCGAGTCAATCAAAAGCAATTCACATGA 1086
QY 1108 CACATGAATTTGGGCTTAACAGTTGCTTCATCTTCAAGGGCACTTACTTCTGACAA 1167
DB 1087 CACATGAATTTGGGCTTAACAGTTGCTTCATCTTCAAGGGCACTTACTTCTGACAA 1146
QY 1168 CAGAGGACATTTGACCTTTTATGGGAAATGATCGTCTTGCTGATATGTGCAATTC 1227
DB 1147 CAGAGGACATTTGACCTTTTATGGGAAATGATCGTCTTGCTGATATGTGCAATTC 1206
QY 1228 TTCTTTGATTTGGATATTTTAAACAGATCATTCGCACTGGGATTTAAAGAAAGATCTTAT 1287
DB 1207 TTCTTTGATTTGGATATTTTAAACAGATCATTCGCACTGGGATTTAAAGAAAGATCTTAT 1266
QY 1288 GTTAATATCAAAAGTGGCTTTATGAAAGATATCTCTAATATGAAAAACAGCAATGTTGTGA 1347
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Db 1267 GTTAATACCAAGTGGCTTATGAGATATCTTAATATGAAAAACGCAATGTTGAA 1326  
Qy 1348 AATGCTACAG 1357  
Db 1327 AATGCTACAG 1336  
RESULT 11  
AA87821  
ID AAF87821 standard; cDNA; 1301 BP.  
XX AAF87821;  
AC  
XX  
XX 11-JUL-2001 (first entry)  
DT  
XX Human haemopoietin receptor protein NR12.4 encoding cDNA SEQ ID NO:7.  
DE  
XX Human haemopoietin receptor protein; NR12; immunosuppressive;  
KM anti-allergic; haemopoietin factor; autoimmune disease; tissue rejection;  
KW metal allergy; pollen allergy; ss.  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FH CDS 1..1287  
FT /tag= a  
FT /product= "NR12.4"  
FT /note= "haemopoietin receptor protein"  
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XX W0200123556-A1.  
XX  
XX PD 05-APR-2001.  
XX  
XX PF 27-SEP-2000; 2000WO-JP006654.  
XX  
XX PR 27-SEP-1999; 99JP-00273358.  
XX PR 03-AUG-2000; 2000JP-00240397.  
XX  
XX (CHUGAI) CHUGAI RES INST MOLECULAR MEDICINE INC.  
XX  
XX Maeda M, Yaguchi N;  
XX  
XX WPI; 2001-266154/27.  
XX P-PDB; AAB74966.  
XX  
XX New hemopoietin receptor protein NR12 useful for screening for new  
PT binding factors for potential treatment of autoimmune disease, tissue  
PT rejection and allergies.  
XX  
XX Claim 1; Fig 11; 140pp; Japanese.  
XX  
XX The present sequence encodes a human haemopoietin receptor protein NR12  
CC designated NR12.4. NR12 has immunosuppressive and anti-allergic  
CC activities. NR12 can be used for searching for haemopoietin factors with  
CC the potential for controlling autoimmune disease, tissue rejection and  
CC allergies against e.g. metals and pollen  
XX  
XX Sequence 1301 BP; 432 A; 253 C; 262 G; 354 T; 0 U; 0 Other;  
SQ  
Query Match 43.3%; Score 1236.6; DB 5; Length 1301;  
Best Local Similarity 99.8%; Pred. No. 7.5e-297;  
Matches 1236; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
Qy 119 ATGAATCACTCACTATTCATGAGATGAGTAATAGCCCTTTACATACCTCTTCAGCTGG 178  
Db 1 ATGAATCAGCTCACTATTCATGAGATGAGTAATAGCCCTTTACATACCTCTTCAGCTGG 60  
Qy 179 TGTCAAGAGAGATTAAATATATAAGTCTGCGCCACATCTGGGTGAACAAGCCACA 238  
Db 61 TGTCAAGAGAGATTAAATATATAAGTCTGCGCCACATCTGGGTGAACAAGCCACA 120  
Qy 239 ATTTTAAAGATGGGTATGAATATCTATATATTGCCAAGCAGCAATTAAGAACTGCCAA 298

Db 121 ATTTTAAAGATGGGTATGAATATCTATATATTGCCAAGCAGCAATTAAGAACTGCCAA 180  
Qy 299 CCAAGAAAGCTCACTTTTATATAAATGGCATCAAGAAAGATTTCAAATCACAAGGATT 358  
Db 181 CCAAGAAAGCTCACTTTTATATAAATGGCATCAAGAAAGATTTCAAATCACAAGGATT 240  
Qy 359 AATTAACAACACAGCTGGCTTTGTATATAAATCTTCTGGAACACATGCTTATGTAC 418  
Db 241 AATTAACAACAGCTGGCTTTGTATATAAATCTTCTGGAACACATGCTTATGTAC 300  
Qy 419 TGCATGCTGAATGTCCCAAACTTTTCAAGAGACATGATATGTGAAAAAGCATTCT 478  
Db 301 TGCATGCTGAATGTCCCAAACTTTTCAAGAGACATGATATGTGAAAAAGCATTCT 360  
Qy 479 TCTGATATCCGCGCAATATCTGATGATGATACCTGTCTATTATGAAATTTTCAGGC 538  
Db 361 TCTGATATCCGCGCAATATCTGATGATGATACCTGTCTATTATGAAATTTTCAGGC 420  
Qy 539 AACATGACTTGCACCTGGAATGTCTGGAAGCTCACCTACATAGACAAATAATGCTGTA 598  
Db 421 AACATGACTTGCACCTGGAATGTCTGGAAGCTCACCTACATAGACAAATAATGCTGTA 480  
Qy 599 CATGTGAAGATTGAAGACAGAAAGACAAAGATATCTCACTCACTATATTATAC 658  
Db 481 CATGTGAAGATTGAAGACAGAAAGACAAAGATATCTCACTCACTATATTATAC 540  
Qy 659 ATCTCCAGATTCATTAACAAGGTGCGCAAGAACTACTGTTGGTTCGCAAGCAAAAC 718  
Db 541 ATCTCCAGATTCATTAACAAGGTGCGCAAGAACTACTGTTGGTTCGCAAGCAAAAC 600  
Qy 719 GCACTAGGACATGGAAGATCAAAACACTGCAATTCACCTGATATATAGTATCT 778  
Db 601 GCACTAGGACATGGAAGATCAAAACACTGCAATTCACCTGATATATAGTATCT 660  
Qy 779 TCTGACCCGCTCAATTCACAGGCTGAGACTATTAATGCTACAGTGCCCAAGCATTAAT 838  
Db 661 TCTGACCCGCTCAATTCACAGGCTGAGACTATTAATGCTACAGTGCCCAAGCATTAAT 720  
Qy 839 TATTGGATATGTAACAACAATTGAAAAGTTTCCCTGTGAATATGATATCAAGGCTACA 898  
Db 721 TATTGGATATGTAACAACAATTGAAAAGTTTCCCTGTGAATATGATATCAAGGCTACA 780  
Qy 899 ACAACCAAACTTGAAATGTTAAAGATTGAACCAATTTTACATATGTGCAACAGTCA 958  
Db 781 ACAACCAAACTTGAAATGTTAAAGATTGAACCAATTTTACATATGTGCAACAGTCA 840  
Qy 959 GAATTCCTTGGAGCCAAACATTAAGTACATTTCAAGTGAATGTCAAGAAACAGGC 1018  
Db 841 GAATTCCTTGGAGCCAAACATTAAGTACATTTCAAGTGAATGTCAAGAAACAGGC 900  
Qy 1019 AAAAGTACTGAGAGCTTGAAGTTGACCGCTTTTTCATATAAACCTGGAACAGTTCCC 1078  
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Qy 1079 CAGGTACATCAAAAGATTCGAACATGACATGGAATCTGGGCTTAACAGTTGCTTC 1138  
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Qy 1139 ATCTTACAGGAGACCTTACTTGTGACACAGAGAGACATTTGATTTATGGGATG 1198  
Db 1021 ATCTTACAGGAGACCTTACTTGTGACACAGAGAGACATTTGATTTATGGGATG 1080  
Qy 1199 ATGCTCTTGGCTGTATATGTGTGAATCTTTCTTTGATTTGGATATTTACATCATTC 1258  
Db 1081 ATGCTCTTGGCTGTATATGTGTGAATCTTTCTTTGATTTGGATATTTACATCATTC 1140  
Qy 1259 CGAAGTGGATTAAGAAGAGATCTTATGTATACAAAGTGGCTTTATGAAGATAT 1318  
Db 1141 CGAAGTGGATTAAGAAGAGATCTTATGTATACAAAGTGGCTTTATGAAGATAT 1200  
Qy 1319 CTTAATATGAAAAACAGCAATGTTGTGAATGCTACAG 1357



KM DNAX cytokine receptor subunit 2; DCRS2; cell physiology;  
KM cell development; cell culture; interferon detection;  
KM immune system disorder; gene; ss.  
XX Homo sapiens.  
OS  
FH Key Location/Qualifiers  
FT CDS 1..1155  
FT /\*tag= a  
FT /product= "DCRS2"  
FT /note= "DNAX cytokine receptor subunit 2"  
XX US2003082734-A1.  
XX 01-MAY-2003.  
XX 18-SEP-2002; 2002US-00247463.  
XX 01-JUN-1999; 99US-0137159P.  
XX 31-MAY-2000; 2000US-00588113.  
XX (DOML/) DOWLING L M.  
XX (TIMA/) TIMANS J C.  
XX (GORM/) GORMAN D M.  
XX (KAST/) KASTELEIN R A.  
XX (BAZA/) BAZAN J F.  
PI Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan JF;  
XX WPI; 2003-730048/69.  
DR P-PSDB; ADC07177.  
XX  
PT Composition potentially useful for treating immunological disorders,  
PT comprises a DNAX cytokine receptor subunit 2 (DCRS2) polypeptide, a  
PT natural DCRS2 polypeptide, or a fusion polypeptide comprising a DCRS2  
PT sequence.  
XX  
PS Claim 16; SEQ ID NO 1; 41pp; English.  
XX  
CC The invention describes a composition of matter (I) comprising a  
CC substantially pure or recombinant DNAX cytokine receptor subunit 2  
CC (DCRS2) polypeptide, a natural DCRS2 polypeptide, or a fusion protein  
CC comprising a DCRS2 sequence. A composition of matter comprises: a  
CC substantially pure or recombinant DCRS2 polypeptide comprising at least  
CC three distinct nonoverlapping segments of at least four amino acids  
CC identical to segments of a fully defined 384 amino acid sequence (S1),  
CC given in the specification; a substantially pure or recombinant DCRS2  
CC polypeptide comprising at least two distinct nonoverlapping segments of  
CC at least five amino acids identical to segments of S1; a natural sequence.  
CC DCRS2 comprising S1; or a fusion polypeptide comprising a DCRS2 sequence.  
CC An agonist or antagonist of a mammalian DCRS2 is useful for modulating  
CC physiology or development of a cell or cell culture. Antibodies to a  
CC DCRS2 can be used for quantitative detection of interferon. The DCRS2  
CC polypeptides and nucleic acids and their binding agents are potentially  
CC useful in treating and diagnosing disease, especially disease associated  
CC with the immune system. This sequence encodes human DNAX cytokine  
CC receptor subunit 2 (DCRS2).  
XX  
SQ Sequence 1155 BP; 387 A; 233 C; 223 G; 312 T; 0 U; 0 Other;  
Query Match 39.9%; Score 1140.6; DB 10; Length 1155;  
Best Local Similarity 99.7%; Pred. No. 5.3e-273;  
Matches 1151; Conservative 2; Mismatches 1; Indels 1; Gaps 1;  
QY 119 ATGAATCACTCACTATTCATGAGATGAGATAGCCCTTACATACCTTCAGCTGG 178  
DB 1 ATGAATCAGGTCACTATTCATGAGATGAGATAGCCCTTACATACCTTCAGCTGG 60  
QY 179 TGTTCATGAGAGATTAACAATATTAATGCTCTGGCCACATCTGGGTAGAACGCCACA 238  
DB 61 TGTTCATGAGAGATTAACAATATTAATGCTCTGGCCACATCTGGGTAGAACGCCACA 120  
QY 239 ATTTTAAGATGGGTATGATATCTCTATATATTGCCAAGAGCAATTAAGAACTGCCAA 298

DB 121 ATTTTAAGATGGGTATGATATCTCTATATATTGCCAAGAGCAATTAAGAACTGCCAA 180  
QY 299 CCAAGGAACCTTATTTTATTAATAATGCAATCAAGAAAGATTTCATACAGAGATT 358  
DB 181 CCAAGGAACCTTATTTTATTAATAATGCAATCAAGAAAGATTTCATACAGAGATT 240  
QY 359 AATTAACAACACAGCTGGCTTTGGTATTAATAAATTCTTGGAACCACTGCTTATGTAC 418  
DB 241 AATTAACAACACAGCTGGCTTTGGTATTAATAAATTCTTGGAACCACTGCTTATGTAC 300  
QY 419 TGCATGCTGAATGTCCTCAAAACATTTTCAAGAGACATGATATGTGAAAAGACATTTCT 478  
DB 301 TGCATGCTGAATGTCCTCAAAACATTTTCAAGAGACATGATATGTGAAAAGACATTTCT 360  
QY 479 TCTGATATCCGCAAGATATCTCTGATGAGATACCTGTCTCAATTAATATTCAGGC 538  
DB 361 TCTGATATCCGCAAGATATCTCTGATGAGATACCTGTCTCAATTAATATTCAGGC 420  
QY 539 AACATGACCTTGACCTGGAATGCTGGAGAGCTCACCTACATAGACAAATAATAGTGTGA 598  
DB 421 AACATGACCTTGACCTGGAATGCTGGAGAGCTCACCTACATAGACAAATAATAGTGTGA 480  
QY 599 CATGTGAAGATTAGAGACAGAAAGAGCAACAGTATCTCACTCAAGCTATATTTAAC 658  
DB 481 CATGTGAAGATTAGAGACAGAAAGAGCAACAGTATCTCACTCAAGCTATATTTAAC 540  
QY 659 ATCTCCACTGATTCATTAACAAGTGGCAGAAAGTACTGTGGTTCAGAGCAAC 718  
DB 541 ATCTCCACTGATTCATTAACAAGTGGCAGAAAGTACTGTGGTTCAGAGCAAC 600  
QY 719 GCATGAGGACATGGAAGATGCAAAACATGCAATTCACCTGATATATAGTATCT 778  
DB 601 GCATGAGGACATGGAAGATGCAAAACATGCAATTCACCTGATATATAGTATCT 660  
QY 779 TCTGACAGCCGTCAATTTCCAGGGCTGAGACTATTAATGCTACAGTCCCAAGACCATTAAT 838  
DB 661 TCTGACAGCCGTCAATTTCCAGGGCTGAGACTATTAATGCTACAGTCCCAAGACCATTAAT 720  
QY 839 TATTGGGATATGTAACAACAATTTGAAAGGTTTCTCTGTAAATGAGATACAGGCTTACA 898  
DB 721 TATTGGGATATGTAACAACAATTTGAAAGGTTTCTCTGTAAATGAGATACAGGCTTACA 780  
QY 899 ACAACCAAACTGGAATGTTAAAGATTGACACCAATTTTCAATATGAGCAACAGTCA 958  
DB 781 ACAACCAAACTGGAATGTTAAAGATTGACACCAATTTTCAATATGAGCAACAGTCA 840  
QY 959 GAATTCATCTTGAGCCAAACATTTAAGTACGATTTTCAAGTGAAGTCAAGAAACAGGC 1018  
DB 841 GAATTCATCTTGAGCCAAACATTTAAGTACGATTTTCAAGTGAAGTCAAGAAACAGGC 900  
QY 1019 AAAAGTACTGAGCAGCTTGGAGTTACCGTTTTCATTAACAACCTGAAACAGTTCCC 1078  
DB 901 AAAAGTACTGAGCAGCTTGGAGTTACCGTTTTCATTAACAACCTGAAACAGTTCCC 960  
QY 1079 CAGGTCAATCAAAACATTTCCAAACATGACATGGAATCTGGGGCTAAAGTTGCTTC 1138  
DB 961 CAGGTCAATCAAAACATTTCCAAACATGACATGGAATCTGGGGCTAAAGTTGCTTC 1020  
QY 1139 ATCTTACAGGGACCTTACTTCTGACAAACAGAGAGACATTTGATTTATTTGGGATG 1198  
DB 1021 ATCTTACAGGGACCTTACTTCTGACAAACAGAGAGACATTTGATTTATTTGGGATG 1080  
QY 1199 ATGCTCTTGGCTGTATATGTTGCAATTTCTTTGATTTGGATATTTAAACAGATCATTT- 1257  
DB 1081 ATGCTCTTGGCTGTATATGTTGCAATTTCTTTGATTTGGGATATTTAAACAGATCATTT- 1140  
QY 1258 CCGAAGCTGGGATTTAA 1272  
DB 1141 CCGAAGCTGGGATTTAA 1155

RESULT 14

ID	ADZ65011	ADZ65011 standard; DNA; 1155 BP.
XX	AC	ADZ65011;
XX	ADZ65011;	
XX	28-JUL-2005	(first entry)
XX	DNAX cytokine receptor subunit 2 (DCRS2) DNA, seq id 1.	
XX	Immunomodulator; cell growth; DNAX cytokine receptor subunits 2; DCRS2;	
XX	immune disorder; gene; ds.	
OS	Primates.	
XX	Key	Location/Qualifiers
FT	CDS	1..1155
FT	/*tag= b	
FT	/product=	"DNAX cytokine receptor subunit 2 (DCRS2)"
FT	sig_peptide	1..69
FT	mat_peptide	/+tag= a
FT		70..1152
FT	/*tag= C	
FT	/product=	"Mature DCRS2"
PN	US2005106673-A1.	
XX	19-MAY-2005.	
PD	17-DEC-2004;	2004US-00016106.
PP	01-JUN-1999;	99US-0137159P.
PR	31-MAY-2000;	2000US-00588113.
PR	18-SEP-2002;	2002US-00247463.
PA	(SCHE ) SCHERING CORP.	
PA	Dowling LM, Timans JC, Gorman DM, Kastellein RA, Bazan JF;	
PI	WPI: 2005-365817/37.	
DR	P-PSDB; ADZ65012.	
XX	Composition useful for diagnosing or treating immunological disorders,	
PT	comprising pure or recombinant DNAX cytokine receptor subunits 2 (DCRS2)	
PT	polypeptide or its fusion polypeptide.	
XX	Disclosure; SEQ ID NO 1; 42bp; English.	
XX	The invention relates to a composition (I) of matter chosen from a	
XX	substantially pure or recombinant DNAX cytokine receptor subunits 2	
CC	(DCRS2) polypeptide. Further disclosed is a substantially pure or	
CC	isolated antigenic DCRS2 polypeptide (II) of (I), a fusion polypeptide	
CC	(III) of (I) and a method for modulating (M1) the physiology or	
CC	development of a cell or tissue culture cells comprising contacting the	
CC	cell with an agonist or antagonist of a mammalian DCRS2. (M1) is useful	
CC	for modulating the physiology or development of a cell or tissue culture	
CC	cells. (II)-(III) are useful for diagnosing or treating immunological	
CC	disorders. The current sequence represents the nucleotide sequence of	
CC	DNAX cytokine receptor subunit 2 (DCRS2).	
XX	Sequence 1155 BP; 387 A; 233 C; 223 G; 312 T; 0 U; 0 Other;	
XX	Query Match	39.9%; Score 1140.6; DB 14; Length 1155;
XX	Best Local Similarity	99.7%; Pred. No. 5.3e-273;
XX	Matches 1151; Conservative	2; Mismatches 1; Indels 1; Gaps 1
0Y	119 ATGAATCAGTCACTATTCAATGAGATGCAAGTAATAGCCCTTACATCTTCAGCTGG	178
Db	1 ATGAATCAGTCACTATTCAATGAGATGCAAGTAATAGCCCTTACATCTTCAGCTGG	60
0Y	179 TGTATGAGAGAAATTACAAATTAAACGCTCTGCGCACATCTGGGTGAACACACCA	238
Db	61 TGTATGAGAGAAATTACAAATTAAACGCTCTGCGCACATCTGGGTGAACACACCA	120

QY	239	ATTTTTAAAGATGGGTAAAGAAATATCTGATATATATATGTCGAAGAGACATTTAAACAATGCGCAA	298
Db	121	ATTTTAAAGATGGGTAAAGAAATATCTCTATATATTTGCCAAGACGACATTTAAGAACTGCGCAA	180
QY	299	CCAAAGAAACTTCATTTTTATATATAAATGGCATCAAGAGATTTCAATCAACAGGATT	358
Db	181	CCAAAGAAACTTCATTTTTATATAAATGGCATCAAGAGATTTCAATCAACAGGATT	240
QY	359	AATTAACAACAGCTCGGCTTTGGTATATAAATCTTCTGGAAACAATGCTCTATATGATC	418
Db	241	AATTAACAACAGCTCGGCTTTGGTATATAAATCTTCTGGAAACAATGCTCTATATGATC	300
QY	419	TGCATGCTGTAATGTCCCAAAACATTTTCAGAGACACTGATATGTGNAAGAACATTTCT	478
Db	301	TGCATGCTGTAATGTCCCAAAACATTTTCAGAGACACTGATATGTGNAAGAACATTTCT	360
QY	479	TCTGGATATCCGCAGATATTTCTGATGAAATTAAGTGTGTCATTTATGAAATATTCAGGC	538
Db	361	TCTGGATATCCGCAGATATTTCTGATGAAATTAAGTGTGTCATTTATGAAATATTCAGGC	420
QY	539	AAACATGACTTGACCTGGAAATGCTRGGAAGTCACTACATAGACACAAAATACGTGGTA	598
Db	421	AAACATGACTTGACCTGGAAATGCTRGGAAGTCACTACATAGACACAAAATACGTGGTA	480
QY	599	CATGTGAAGATTTAGAGACAGAAAGAAAGCAACGATATCTCACTCAAGCTATATTAAC	658
Db	481	CATGTGAAGATTTAGAGACAGAAAGAAAGCAACGATATCTCACTCAAGCTATATTAAC	540
QY	659	ATCTCCACTGATTCATATCAAAAGGTGGCAAGAAAGTACTTGTTGGTTCAGACAGCAAC	718
Db	541	ATCTCCACTGATTCATATCAAAAGGTGGCAAGAAAGTACTTGTTGGTTCAGACAGCAAC	600
QY	719	GCACCTAGGCAATGGAAGAGTCAAAAACACTGCAGAAATTCACCTGATATGATATGATACCT	778
Db	601	GCACCTAGGCAATGGAAGAGTCAAAAACACTGCAGAAATTCACCTGATATGATATGATACCT	660
QY	779	TCTGAGCGGTCATTTCCAGGGCTGAGACTATAATGCTACAGTGGCCCAAGACCATTAAT	838
Db	661	TCTGAGCGGTCATTTCCAGGGCTGAGACTATAATGCTACAGTGGCCCAAGACCATTAAT	720
QY	839	TATTTGGGATAGTCAAAACAATTTGAAAGGTTCTGTGAATATGAGATACAGGCTACAG	898
Db	721	TATTTGGGATAGTCAAAACAATTTGAAAGGTTCTGTGTGAATATGAGATACAGGCTACAG	780
QY	899	ACAAACCAAACTTGGAATGTTAAAGAAATTTGACACAAATTTACATATGTGCAACAGTCA	958
Db	781	ACAAACCAAACTTGGAATGTTAAAGAAATTTGACACCAATTTTACATATGTGCAACAGTCA	840
QY	959	GAATTTTACTTTGGAGCCAAACATTTAATGTAAGTATTTCAAGAGATATGCAAGAAACAGGC	1018
Db	841	GAATTTTACTTTGGAGCCAAACATTTAATGTAAGTATTTCAAGAGATATGCAAGAAACAGGC	900
QY	1019	AAAAGTACTGGCAGCCTTGAGATTTCAACCGTTTTCATATAACAACCTGAACAGTTCCC	1078
Db	901	AAAAGTACTGGCAGCCTTGAGATTTCAACCGTTTTCATATAACAACCTGAACAGTTCCC	960
QY	1079	CAGGTCACATCAAAAGCATTTCCAAACATGACACATGGAATTTCTGGGCTTAACAGTTGCTCC	1138
Db	961	CAGGTCACATCAAAAGCATTTCCAAACATGACACATGGAATTTCTGGGCTTAACAGTTGCTCC	1020
QY	1139	ATCTCTACAGGGCACTTACTCTTCTGACACAGAGAGACATTTGAATTGGAATG	1198
Db	1021	ATCTCTACAGGGCACTTACTCTTCTGACACAGAGAGACATTTGAATTGGAATG	1080
QY	1199	ATCGCTCTTGTGCTGTTATGTTGTCAATCTTTCTTTGATTGGGAATATTTAACAGATCATTT	1257
Db	1081	ATCGCTCTTGTGCTGTTATGTTGTCAATCTTTCTTTGATTGGGAATATTTAACAGATCATTT	1140
QY	1258	CCGAACCTGGGATTTAA 1272	
Db	1141	CCGAACCTGGGATTTAA 1155	

RESULT 15  
AAD38777  
ID AAD38777 standard; DNA, 1935 BP.  
XX  
AC AAD38777;  
XX  
DT 23-SEP-2002 (first entry)  
XX  
DE Mouse haematopoietin receptor 2 (HPR2) DNA.  
XX  
KM Mouse; haematopoietin receptor; receptor; HPR1; HPR2; cell proliferation;  
KM pancytopenia; leukopenia; anaemia; thrombocytopaenia; osteoporosis;  
KM neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder;  
KM cancer; myeloid myeloid syndrome; idiopathic thrombocytopenic purpura;  
KM ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;  
KM osteoclast disorder; periodontitis; acute polyneuropathy; Bell's palsy;  
KM demyelinating neuropathy; Guillain-Barre syndrome; Creutzfeldt-Jacob disease;  
KM amyotrophic lateral sclerosis; chronic fatigue syndrome; Gulf war syndrome;  
KM vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;  
KM stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;  
KM ischaemic disease; gene; ds.  
XX  
OS Mus musculus.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1935  
FT /tag= a  
FT /product= "Mouse HPR2 protein"  
XX  
PN MO200229060-A2.  
XX  
PD 11-APR-2002.  
XX  
PF 05-OCT-2001; 2001MO-US031634.  
XX  
PR 06-OCT-2000; 2000US-0238706P.  
PR 13-OCT-2000; 2000US-0240476P.  
PR 20-FEB-2001; 2001US-0270282P.  
XX  
PA (IMMUNEX CORP.  
XX  
PI Cosman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR;  
XX  
DR WPI: 2002-330172/36.  
DR P-PSDB; AAE24038.  
XX  
XX Human and murine haematopoietin receptor polypeptides HPR1 and HPR2,  
PT useful for treating cell proliferation, metabolic, and reproductive  
PT hormone related conditions.  
XX  
PS Claim 9; Page 135-136; 136pp; English.  
XX  
XX The present invention relates to human and murine haematopoietin receptor  
CC polypeptides HPR1 and HPR2. Sequences of the invention are useful for  
CC treating cell proliferation conditions e.g., pancytopenia, leukopenia,  
CC anaemia, thrombocytopenia, neurodegenerative disorders and osteoporosis  
CC resulting from a lack of bone-forming cells. They are also useful for  
CC treating cell proliferation conditions such as leukaemia and tumour  
CC metastasis, osteoporosis resulting from an excess of bone-resorbing  
CC cells. HPR sequences are also useful for treating medical conditions and  
CC diseases such as cell proliferation, metabolic and reproductive hormone  
CC related conditions. They are useful for treating various haematologic and  
CC oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal  
CC carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell,  
CC cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including  
CC cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma,  
CC squamous cell carcinoma (e.g., adenocarcinoma (for example, breast cancer),  
CC sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer),  
CC of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelo-  
CC dysplastic syndromes (including refractory anaemia, refractory anaemia  
CC with ringed sideroblasts or with excess blasts), idiopathic thrombocy-  
CC penic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/  
CC myeloid metaplasia, osteoclast disorders that lead to bone loss such as

CC osteoporosis including post-menopausal osteoporosis, periodontitis  
CC resulting in tooth loosening or loss, prosthesis loosening after joint  
CC replacement, neurodegenerative conditions (e.g., acute polyneuropathy,  
CC Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible  
CC dementia including Creutzfeldt-Jacob disease, demyelinating neuropathy,  
CC Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome,  
CC myasthenia gravis, chronic neuronal degeneration, stroke including  
CC cerebral ischaemic diseases. HPR1 and HPR2 polypeptides are also useful  
CC for treating various other disorders such as osteoporosis, obesity,  
CC deficient mammary development and infertility. The present sequence is  
CC mouse HPR2 DNA  
XX  
SQ Sequence 1935 BP; 607 A; 420 C; 385 G; 523 T; 0 U; 0 Other;  
Query Match 38.7%; Score 1105.8; DB 6; Length 1935;  
Best Local Similarity 75.2%; Pred. No. 2.9e-264;  
Matches 1468; Conservative 1; Mismatches 403; Indels 81; Gaps 4;  
QY 119 ATGATCACTGCTCACTATTCATGAGATGAGTATAGCCCTTACATACCTCTGAGCTGG 178  
DB 1 ATGAGTCACTGCTCACTGCTGAGTATGCTGATGCTTATATGCTCTTCAATGAG 60  
QY 179 TGTATGAGAGAAATTACAAATATTAATCTGCTGAGCACTGAGGATGAGCAACA 238  
DB 61 TGTACGAGAGAAATCAACAGTATTAATCTGCTGAGCACTGAGGATGAGCAACA 120  
QY 239 ATTTTAAAGTGGATGAAATATCTATATATGCTGAGCACTGAGGATGAGCAACA 298  
DB 121 ATTTTCAAGTGGATGAAATATCTATATATGCTGAGCACTGAGGATGAGCAACA 180  
QY 299 CCAAGGAACTGCTATTTTAAATATGAGTATGAGTATGAGTATGAGTATGAGTAT 358  
DB 181 CCAAGGAACTGCTATTTTAAATATGAGTATGAGTATGAGTATGAGTATGAGTAT 240  
QY 359 AATTAACCAAGCTGCTGCTTGTATTAATATTTTGAACCACTGCTTATATATAC 418  
DB 241 AATTAACCAAGCTGCTGCTTGTATTAATATTTTGAACCACTGCTTATATATAC 300  
QY 419 TGCACTGCTGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 478  
DB 301 TGCACTGCTGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
QY 479 TCTGATATCCGAGATATTTCTGATATGAGTATGAGTATGAGTATGAGTATGAGT 538  
DB 361 TCTGATATCCGAGATATTTCTGATATGAGTATGAGTATGAGTATGAGTATGAGT 420  
QY 539 AACATGATCTGCACTGAGATGCTGAGATGCTGAGATGCTGAGATGCTGAGATGCT 598  
DB 421 AACATGATCTGCACTGAGATGCTGAGATGCTGAGATGCTGAGATGCTGAGATGCT 480  
QY 599 CATGTGAAGGTTTAAAG 658  
DB 481 CATGTGAAGGTTTAAAG 540  
QY 659 ATTCATGATCTGATTAATCAAGTATGAGTATGAGTATGAGTATGAGTATGAGTAT 718  
DB 541 ATTCATGATCTGATTAATCAAGTATGAGTATGAGTATGAGTATGAGTATGAGTAT 600  
QY 719 GCACTGAGGATGAG 778  
DB 601 TCCTTGAAGGATGAG 660  
QY 779 TCTGAGAGGATGAG 838  
DB 661 TCTGAGAGGATGAG 720  
QY 839 TATTTGATGATGAG 898  
DB 721 TATTTGATGATGAG 780  
QY 899 ACAATCAAGGATGAG 958  
DB 781 ACAATCAAGGATGAG 840

QY 959 GAACTTCTACTGGAGCCAAACATTAAGTATTTCAAGTGAATGTCAGAAACAGGC 1018  
 DB 841 GAACTTCTACTGGAGCCAGACAGCAAGTATGATTTCAAGTGAATGTCAGAAACAGGC 900  
 QY 1019 AAAAGTACTGGAGCTTGGAGTTCACCGTTTTCATTAACACCTGAA----- 1069  
 DB 901 AAAAGAACTGGAGCTTGGAGTTCACCGTTTTCATTAACACCTGAACTGCT 960  
 QY 1070 -----ACAGTTCC 1078  
 DB 961 AAAAGAACTGGAGCTTGGAGTTCACCGTTTTCATTAACACCTGAACTGCT 1020  
 QY 1079 CAGTCAATCAAAAGCATTCACATGACATGAAATTCGGCTTACAGTTGCTTCC 1138  
 DB 1021 CAGGTTACAGCAAAATCATCC---CAGGAACCTCAGAAATGAGATGTCAGTGTACA 1077  
 QY 1139 ATCTCTACAGGAGCACTTACTTCTGACACAGAGAGACATGACCTTTTATTTGGAAATG 1198  
 DB 1078 ATCTCTACAGGAGCACTTACTTCTGACATCAAGACATGAACTTGTGCGGAATG 1137  
 QY 1199 ATGCTCTTGTCTGTATTTGTTCAATCTTCTTGTGGAATTTAATTAAGATTC 1258  
 DB 1138 GTCTTCTTGGCCATCATGTTGGATTTTCTCTGATTTGGATTTTAACATCACTT 1197  
 QY 1259 CGAATCTGGATTTAAAGAAAGATCTTATGTTAATACAAAGTGGCTTTATGAAGATTT 1318  
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 QY 1319 CCTAATATGAAAAAAGCAATGTTTGAATAATGCTACAGAAATAGTGAATTAATGAAT 1378  
 DB 1258 CCTAATATGAAAAAAGCAATGTTTGAATAATGCTACAGAAATAGTGAATTTGAAT 1317  
 QY 1379 AATATTTCCAGTGAAGCTATATATGTTGATCCCATGATTAAGATTAAGAAATC 1438  
 DB 1318 GATTAATCCAGTGAAGCTATATATGTTGATCCCATGATTAAGATTAAGAAATC 1377  
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 DB 1378 TCTCCCTGGAAACAAACCAAGATTAAGAAAGAAAGCTCACAGATCTCTTGAG 1437  
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 DB 1438 ACAAGAGCTATGCTCTTGAAGATGTTGCTACAGATCTCTGATTAATTTCTGAC 1497  
 QY 1556 CTCACACTGATATTAACCCCAATTTTCAATTTTCTGCTGAGGAGCACTCAGC 1615  
 DB 1498 CTCACACTGATATTAACCCCAATTTTCAATTTTCTGCTGAGGAGCACTTTTCAAT 1557  
 QY 1616 AATATATGAATTAATCTTCACTTAACCTTAAACCAAGTGAATTCCTTGAAGCA 1675  
 DB 1558 AACAGAGATGAAGAGACCTTACATCCCTTGAAGCAAGATGACACTT----- 1607  
 QY 1676 AATATATCCAGGTTACAAAGCATCTTAATTTTCTGCTTCTGTTCAAGTGAATTC 1735  
 DB 1608 -----TGCCGATTTGAAGAAATATCCCACTTCAATTTTCTGCTTCAAGTGAATTC 1662  
 QY 1736 CTAAGCAACATTAATTTCTTGAAGATTAAGCTCATTAATTAATCAAGGAGATGAGT 1795  
 DB 1663 CTAAGCAACATTAATTTCTTGAAGATTAAGCTCATTAATTAATCAAGGAGATTCAT 1722  
 QY 1796 TCTCTGACATTAACAACTGATGAGAGAAACCAATGCTTTTGAAGAAATGATTC 1855  
 DB 1723 TCTCTGACATTAACAACTGATGAGAGAAACCAATGCTTTTGAAGAGATGATTC 1782  
 QY 1856 CCAAGTGAATCTTTCGAAACAGACCTGCTTCTGATGAATTTGCTCTGTTGGGG 1915  
 DB 1783 CCAAGTGAATCTTTCGAAACAGACCTGCTTCTGATGAATTTGCTCTGTTGGCA 1842  
 QY 1916 ATGATGAATGAGAGTTCATTAATTAATTAATTTTCACAAAATATTTTGAAGAGC 1975  
 DB 1843 ATGATGAATGAGAGTTCATTAATTAATTAATTTTCACAAGAGTTCGTAAGAGC 1902

QY 1976 CACTTCAATGAGATTTCACTCTTGGAAAAAGTAG 2008  
 DB 1903 CACTTCAATGAGATTTCACTCTTGGAAAAAGTAG 1935  
 Search completed: October 14, 2006, 12:53:55  
 Job time : 1724 secs







Oy	2341	GGTCCCGAAGGTGGAAACATGCTTCATGCTGCACATTAAGGCAAAAAACAGCATTTATGT	2400
Db	2341	GGTCCCGAAGGTGGAAACATGCTTCATGCTGCACATTAAGGCAAAAAACAGCATTTATGT	2400
Oy	2401	GGAGCGCTCATGTATTTTATAGAGTCACATATTTCTCTTTATTTTCCCTCATTTGAA	2460
Db	2401	GGAGCGCTCATGTATTTTATAGAGTCACATATTTCTCTTTATTTTCCCTCATTTGAA	2460
Oy	2461	GATGCAAAACAGCTCTCTATTTGTGTACAGAAAGGTAATATATGCAAAATATCTGTGATG	2520
Db	2461	GATGCAAAACAGCTCTCTATTTGTGTACAGAAAGGTAATATATGCAAAATATCTGTGATG	2520
Oy	2521	AAATTAATATGCTGAAAATTTTCTTTAATATGAAATCATTTAGGCGAGGCGTGTGCTCA	2580
Db	2521	AAATTAATATGCTGAAAATTTTCTTTAATATGAAATCATTTAGGCGAGGCGTGTGCTCA	2580
Oy	2581	TGCTTGTATATCCACAGCATTTTGATGTAGGCTGAGTGTGATCATCTGAGTCAAGGTT	2640
Db	2581	TGCTTGTATATCCACAGCATTTTGATGTAGGCTGAGTGTGATCATCTGAGTCAAGGTT	2640
Oy	2641	CGAGTCCAGCCTGCGCAATATGCTGAAAACCTGTCTCTACTAATAATTGCAAAATTTAGCC	2700
Db	2641	CGAGTCCAGCCTGCGCAATATGCTGAAAACCTGTCTCTACTAATAATTGCAAAATTTAGCC	2700
Oy	2701	GGCCATGCTGCGCAGGTGCTTGTATATCCAGCTACTTGGAGGCTGAGGACAGAAATTCAC	2760
Db	2701	GGCCATGCTGCGCAGGTGCTTGTATATCCAGCTACTTGGAGGCTGAGGACAGAAATTCAC	2760
Oy	2761	TTGAACACGGAAGGACAGAGTTGCACTGAGCTGAGATTGTGCCACTGCACTCCAGCCTGG	2820
Db	2761	TTGAACACGGAAGGACAGAGTTGCACTGAGCTGAGATTGTGCCACTGCACTCCAGCCTGG	2820
Oy	2821	GCAACAAAGACAAAATCTGTGCTGGAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTT	2859
Db	2821	GCAACAAAGACAAAATCTGTGCTGGAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTT	2859
RESULT 2			
US-10-797-157-5			
; Sequence 5, Application US/10797157			
; Publication No. US2004023969A1			
; GENERAL INFORMATION:			
; APPLICANT: McClanahan, Terrill K.			
; TITLE OR INVENTION: USES OF IL-23 AGONISTS AND ANTAGONISTS; RELATED REAGENTS			
; FILE REFERENCE: DX06022U0501			
; CURRENT APPLICATION NUMBER: US/10797, 157			
; CURRENT FILING DATE: 2004-03-09			
; PRIOR APPLICATION NUMBER: U.S. 60/453,672			
; PRIOR FILING DATE: 2003-03-10			
; NUMBER OF SEQ ID NOS: 11			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 5			
; LENGTH: 2859			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (119)..(2005)			
; FEATURE:			
; NAME/KEY: mat peptide			
; LOCATION: (188)..(2005)			
US-10-797-157-5			

Query Match	100.0%	Score 2857.4;	DB 9;	Length 2859;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2859; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;
Oy	1	GTGGTACCGGAATTCATTGTTGTGGGCAGCAACAAGGCTGGAGCCTCGAAGT	60	
Dd	1	GTGGTACCGGAATTCATTGTTGTGGGCAGCCAAAGGCTGGAGCCTCGAAGT	60	

OY	6	GGAAATTATGTCCTCAAAACAGTGTGAAAGAGGAAA	CAGTCTTTTCCGTCTCCAGACAT	120
Db	61	GGAAATTATGTCCTCAAAACAGTGTGAAAGAGGAAA	CAGTCTTTTCCGTCTCCAGACAT	120
OY	121	GAATCAGTCACTATTCATATGGGATGCGATATAGCC	CTTTACATCTTCAGCTGGTG	180
Db	121	GAATCAGTCACTATTCATATGGGATGCGATATAGCC	CTTTACATCTTCAGCTGGTG	180
OY	181	TCATGAGGAAATTACAAATATATACTGTCTGAGAT	TCGGGTGAGAACGACCAAT	240
Db	181	TCATGAGGAAATTACAAATATATACTGTCTGAGAT	TCGGGTGAGAACGACCAAT	240
OY	241	TTTTAAGTGGGTATGAAATATCTATATATTCGCA	GACACAAATTAGAACTGGCAAC	300
Db	241	TTTTAAGTGGGTATGAAATATCTATATATTCGCA	GACACAAATTAGAACTGGCAAC	300
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Db	301	AAGGAACTCATTTTATATATAAATATGGCATCAA	AGAAAAGATTCCAAATCAAGAGATTAA	360
OY	361	TAAACAAACAGCTCGGCTTTGGTATATAAACTTT	CTGGAAACACATGCTTCTATGTACTG	420
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OY	421	CACGTCTGAATGTCCCAACACTTTTCAAGAGAC	ACTGATATGTGGAAAAGACATTTCTTC	480
Db	421	CACGTCTGAATGTCCCAACACTTTTCAAGAGAC	ACTGATATGTGGAAAAGACATTTCTTC	480
OY	481	TGGATATCCGCGAGATATCTGTATGAAAGTAA	CCGTGTCATTTATGAATATTCAGGCAA	540
Db	481	TGGATATCCGCGAGATATCTGTATGAAAGTAA	CCGTGTCATTTATGAATATTCAGGCAA	540
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Db	541	CATGACTTGCACCTGGAATGCTRGGAACTCAC	CTACATAGACACAAATAATCGTGTACA	600
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Db	601	TGTGAAGAATTATAGAGACAGAAAGAGCA	CAGTATCTCACTCCAGCTATATTAACAT	660
OY	661	CTCAGCTGAATCATTAACAAGTGGCAAGAACT	ACTGTGTTGGGTCCAAAGACGAAAGC	720
Db	661	CTCAGCTGAATCATTAACAAGTGGCAAGAACT	ACTGTGTTGGGTCCAAAGACGAAAGC	720
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OY	781	TGCAGCGGTCAATTTCCAGGGCTGAGACTATA	ATAATGCTACAGTGCCCAAGACATATTTA	840
Db	781	TGCAGCGGTCAATTTCCAGGGCTGAGACTATA	ATAATGCTACAGTGCCCAAGACATATTTA	840
OY	841	TTGGGATGTCAAAACAATTGAAAAGGTTTCT	GTAAGATGAGATCAAGGCTTACAC	900
Db	841	TTGGGATGTCAAAACAATTGAAAAGGTTTCT	GTAAGATGAGATCAAGGCTTACAC	900
OY	901	AAACCAAACTTGAATGTTAAAGATTGACACCA	ATTTTCAATATGTCACACAGTCA	960
Db	901	AAACCAAACTTGAATGTTAAAGATTGACACCA	ATTTTCAATATGTCACACAGTCA	960
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Db	961	ATTCTACTTGGAGCAAACTTAATAGTACGTAT	TTCAAATGAGATGTCAGAAACAGCAA	1020
OY	1021	AAGGTATCTGGAGCCAAACTTAATAGTACGTAT	TTCAAATGAGATGTCAGAAACAGCAA	1080
Db	1021	AAGGTATCTGGAGCCAAACTTAATAGTACGTAT	TTCAAATGAGATGTCAGAAACAGCAA	1080
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2761 TTGAACAGAGAGAGAGAGGTGACATGAGTGAATTTGAGCACTGCACTCCAGCTGGA 2820  
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2821 GCAACAGAGCAAACTGCTGCTGAGAAAAAATTTTAAAAA 2859

RESULT 3  
US-10-720-026-1  
; Sequence 1, Application US/10720026  
; Publication No. US2004025868A1  
; GENERAL INFORMATION:  
; APPLICANT: Chitica, Madeline  
; APPLICANT: Parham, Christi L.  
; APPLICANT: Kastelein, Robert A.  
; APPLICANT: Moore, Kevin W.  
; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods.  
; PIR REFERENCE: DQ01074B1K  
; CURRENT APPLICATION NUMBER: US/10/720, 026  
; CURRENT FILING DATE: 2003-11-21  
; PRIOR APPLICATION NUMBER: 60/203, 426  
; PRIOR FILING DATE: 2000-05-10  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 2859  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (119)..(2005)  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: (188)..(2005)  
US-10-720-026-1

Query Match 100.0%; Score 2857.4; DB 9; Length 2859;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2859; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GTGTCACGGAATTCCTTGTGTGGGACCCACCAAGGGTGGCAGCTGCTGTAAGT 60  
QY 61 GGAATTAATGCTCTCAACAGGTTGAAAGAGGAAACAGCTCTTCTGCTCCAGCAT 120  
DB 61 GGAATTAATGCTCTCAACAGGTTGAAAGAGGAAACAGCTCTTCTGCTCCAGCAT 120  
QY 121 GAATCAAGTCACTATTCATAGGATGAGTAAATAGCCCTTATCATATCTTCAAGCTG 180  
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QY 181 TCATGAGGAAATTAACAATATAAATCTGCTGCGCACATCTGGGTAGAACCCAGCAAT 240  
DB 181 TCATGAGGAAATTAACAATATAAATCTGCTGCGCACATCTGGGTAGAACCCAGCAAT 240  
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DB 2041 GCTTGAATCTGAACCTTGGGTTTTTCCCTGCAATTAAGAAATGCAATCTGCTTTTGA 2100  
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# RESULT 4 US-10-667-289-1

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; Sequence 1, Application US/10667289
; Publication No. US20050100917A1
; GENERAL INFORMATION:
; APPLICANT: Chirica, Madeline
; APPLICANT: Parham, Christi L.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Moore, Kevin W.
; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods.
; FILE REFERENCE: D010174
; CURRENT APPLICATION NUMBER: US/10/667,289
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/853,180
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,426
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent version 3.2
; SEQ ID NO 1
; LENGTH: 2859
; TYPE: DNA
; ORGANISM: Homo sapiens

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; NAME/KEY: CDS
; LOCATION: (119) .. (2005)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (127) .. (127)
; OTHER INFORMATION: k means g or t/u. See page 12, line 34, of patent application 48
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: (188) .. (2005)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (563) .. (563)
; OTHER INFORMATION: r means g or a. See page 12, line 36, of patent application as
; OTHER INFORMATION: originally filed.
; US-10-667-289-1

Query Match 100.0%; Score 2857.4; DB 10; Length 2859;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2859; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5  
 US-10-667-290-1  
 ; Sequence 1, Application US/10667290  
 ; Publication No. US20050100918A1

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GENERAL INFORMATION:
APPLICANT: Chirica, Madeline
APPLICANT: Parham, Christi L.
APPLICANT: Kastelein, Robert A.
APPLICANT: Moore, Kevin W.
TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods.
FILE REFERENCE: DX01074
CURRENT APPLICATION NUMBER: US/10/667,290
CURRENT FILING DATE: 2003-09-18
PRIORITY APPLICATION NUMBER: US/09/853,180B
PRIORITY FILING DATE: 2001-05-10
PRIORITY APPLICATION NUMBER: 60/203,426
PRIORITY FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 2859
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: CDS
LOCATION: (119)..(2005)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (127)..(127)
OTHER INFORMATION: k means g or t/u. See page 12, line 34, of patent application as
OTHER INFORMATION: originally filed.
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (188)..(2005)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (563)..(563)
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US-10-667-290-1

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Query Match 100.0%; Score 2857.4; DB 10; Length 2859;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2859; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6  
US-09-972-708-19  
; Sequence 19, Application US/09972708  
; Publication No. US20030059871A1  
; GENERAL INFORMATION:  
; APPLICANT: Immunex Corporation  
; APPLICANT: Cosman, David J.  
; APPLICANT: Mosley, Bruce A.  
; APPLICANT: Bird, Timothy A.  
; APPLICANT: Dubose, Robert F.  
; APPLICANT: Wiley, Steven R.  
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2  
; FILE REFERENCE: 3160-B  
; CURRENT APPLICATION NUMBER: US/09/972,708  
; CURRENT FILING DATE: 2001-10-05  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 2830  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-09-972-708-19  
Query Match 98.3%; Score 2810.2; DB 3; Length 2830;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 2809; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
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DB 1456 CAAGAAAGAGATTAACAGAGCCCTGTGAGAGACAGAGCTAACCCGCAAACTGCTATTGGA 1515  
QY 1528 CAATACAGAGTTGATATATATCTGATCTCAACACTGGAATTAATTAACCCCAATTTGAAA 1587  
DB 1516 CAATACAGAGTTGATATATATCTGATCTCAACACTGGAATTAATTAACCCCAATTTGAAA 1575

QY 1588 TTTTCCTGAGGAGAGCCATCTCAGCAATATATTAAGAAATTAATCTTCTTAACACTTAA 1647  
DB 1576 TTTTCCTGAGGAGAGCCATCTCAGCAATATATTAAGAAATTAATCTTCTTAACACTTAA 1635  
QY 1648 ACCACAGTTGAATCTTGAAGCTCAGAGAAATTAATCCAGGTTTACAAAGACATCTTAATT 1707  
DB 1636 ACCACAGTTGAATCTTGAAGCTCAGAGAAATTAATCCAGGTTTACAAAGACATCTTAATT 1695  
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QY 1768 CCTCATTAATTAACAGAGAAATGCACTTCTCTGACATTAACAAATCTCAGTAGAGAGA 1827  
DB 1756 CCTCATTAATTAACAGAGAAATGCACTTCTCTGACATTAACAAATCTCAGTAGAGAGA 1815  
QY 1828 AACACAGCTTTTGGAAAAATGATCACCCAGTGAACATATTCAGAAACAGACCTGCT 1887  
DB 1816 AACACAGCTTTTGGAAAAATGATCACCCAGTGAACATATTCAGAAACAGACCTGCT 1875  
QY 1888 TCCGTGATGAATTTGCTCCTGTTTGGGATTCGTGAATGAGAGTTGCCATTAATTAAC 1947  
DB 1876 TCCGTGATGAATTTGCTCCTGTTTGGGATTCGTGAATGAGAGTTGCCATTAATTAAC 1935  
QY 1948 TTAATTTCCACAAATATTTTGGAAAGCACTTCAATAGAAATTCCTTGGAAAAAGTA 2007  
DB 1936 TTAATTTCCACAAATATTTTGGAAAGCACTTCAATAGAAATTCCTTGGAAAAAGTA 1995  
QY 2008 GAGCTGTGTGTCAAATTAATTAATGAGAAAGCTGCTGCAATCTGAACCTGGGTTTCC 2067  
DB 1996 GAGCTGTGTGTCAAATTAATTAATGAGAAAGCTGCTGCAATCTGAACCTGGGTTTCC 2055  
QY 2068 CTGCAATAGAAATTTGAAATCTGCTCTTTTGGAAAAATTAATTAATTAATTAATTAAT 2127  
DB 2056 CTGCAATAGAAATTTGAAATCTGCTCTTTTGGAAAAATTAATTAATTAATTAATTAAT 2115  
QY 2128 ACATGACACATGTTTCAATTTCCCTTGGATTAATCTTAAGTAAAGGATGCTGGGCA 2187  
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QY 2188 TATGATAGCATATGTTTCAATTTCCCTTGGATTAATCTTAAGTAAAGGATGCTGGG 2247  
DB 2176 TATGATAGCATATGTTTCAATTTCCCTTGGATTAATCTTAAGTAAAGGATGCTGGG 2235  
QY 2248 CTCCTACATCAACATGTAAGAAATCCCGAGGCTCCATGCTTTTAAATTTAGCCATT 2307  
DB 2236 CTCCTACATCAACATGTAAGAAATCCCGAGGCTCCATGCTTTTAAATTTAGCCATT 2295  
QY 2308 CTTCTGCTMAATTTCTTAAATTTAGAAATTAAGGATCCGAAAGTGAACATGCTTCAATG 2367  
DB 2296 CTTCTGCTMAATTTCTTAAATTTAGAAATTAAGGATCCGAAAGTGAACATGCTTCAATG 2355  
QY 2368 GTACACATTAACAGGCAAAAACAGATTAATGAGAGGCTCATGATTTTAAATTAAGAGT 2427  
DB 2356 GTACACATTAACAGGCAAAAACAGATTAATGAGAGGCTCATGATTTTAAATTAAGAGT 2415  
QY 2428 CAATATTTCTCTTATTTTCCCTCATGAAAGATGCAAAACAGCTCTCATATGTTGATC 2487  
DB 2416 CAATATTTCTCTTATTTTCCCTCATGAAAGATGCAAAACAGCTCTCATATGTTGATC 2475  
QY 2488 AGAAAGGTAATTAATGCAAAATACCTGATGTAATTAATTAATGCTGAAAAATTTCTTTA 2547  
DB 2476 AGAAAGGTAATTAATGCAAAATACCTGATGTAATTAATTAATGCTGAAAAATTTCTTTA 2535  
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DB 2536 AAATTAATTAATTAAGGCAAGGCTGTGCTCATGCTTAATCCAGACCTTTGGTAGG 2595  
QY 2608 CTGAGGTGATGATCACTGAGGTGAGAGTTCAGAGTCCAGGCTGGCAATATGCTGAA 2667  
DB 2596 CTGAGGTGATGATCACTGAGGTGAGAGTTCAGAGTCCAGGCTGGCAATATGCTGAA 2655  
QY 2668 ACCCTGTCTCTAATAATTAACAAAAATTAAGCCGAGCATGATGGCAGGTGCTTGTAACTC 2727

Db 2656 ACCCTGCTCTACTAAATTAATCAAAAAATTACCCGCCCATGCTGGCAGGTGCTTAAATCC 2715  
Qy 2728 CAGTACTTGGGAGGCTGAGCAGAGAAATCACTTGAACCCAGGAAGCAGAGTTGCACT 2787  
Db 2716 CAGTACTTGGGAGGCTGAGCAGAGAAATCACTTGAACCCAGGAAGCAGAGTTGCACT 2775  
Qy 2788 GAGCTGAGATTGTGCCACTGCACTCCAGCCTGGCAACAAGCAAAACTCTGTC 2842  
Db 2776 GAGCTGAGATTGTGCCACTGCACTCCAGCCTGGCAACAAGCAAAACTCTGTC 2830

## RESULT 7

US-10-715-667-19  
; Sequence 19. Application US/10715667  
; Publication No. US20040152161A1  
; GENERAL INFORMATION:  
; APPLICANT: Immunex Corporation  
; APPLICANT: Mosley, David J.  
; APPLICANT: Mosley, Bruce A.  
; APPLICANT: Bird, Timothy A.  
; APPLICANT: Dubose, Robert F.  
; APPLICANT: Wiley, Steven R.  
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2  
; FILE REFERENCE: 3160-B  
; CURRENT APPLICATION NUMBER: US/10/715,667  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: US/09/972,708  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 2830  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-715-667-19

Query Match 98.3%; Score 2810.2; DB 8; Length 2830;

Best Local Similarity 99.8%; Pred. No. 0; Matches 2809; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 28 CAGCCAAACAAGGCTGGAGCGCTGCTGAAGTGAATTAATGCTTCAACAGGTGAA 87  
Db 16 CAGCCAAACAAGGCTGGAGCGCTGCTGAAGTGAATTAATGCTTCAACAGGTGAA 75  
Qy 88 AGAGGGAACAGTCTTTTCTGCTTCCAGACATGATCACTCACTATTCATGGAATGC 147  
Db 76 AGAGGGAACAGTCTTTTCTGCTTCCAGACATGATCACTCACTATTCATGGAATGC 135  
Qy 148 AGTAATAGCCCTTAACTACTCTTCACTGCTGTCATGAGGAATTAATAATAATCTG 207  
Db 136 AGTAATAGCCCTTAACTACTCTTCACTGCTGTCATGAGGAATTAATAATAATCTG 195  
Qy 208 CTCTGGCAGATCTGGGTAGAACAGCCACAATTTTAAAGTGGTATGAATATCTCTAT 267  
Db 196 CTCTGGCAGATCTGGGTAGAACAGCCACAATTTTAAAGTGGTATGAATATCTCTAT 255  
Qy 268 ATATTTGCCAAGCAGCAATTAAGAACTGCCAACCAAGAAACTTCAATTTTATAAAAAATGG 327  
Db 256 ATATTTGCCAAGCAGCAATTAAGAACTGCCAACCAAGAAACTTCAATTTTATAAAAAATGG 315  
Qy 328 CATCAAGAAAGAAATTTCAATCAACAAGATTAATAAACAACAGCTGGCTTGGTATAA 387  
Db 316 CATCAAGAAAGAAATTTCAATCAACAAGATTAATAAACAACAGCTGGCTTGGTATAA 375  
Qy 388 AAATCTTCTGGAAACCAATGCTTATATGATCTGCACTGCTGAATGCTCCAAACATTTTCA 447  
Db 376 AAATCTTCTGGAAACCAATGCTTATATGATCTGCACTGCTGAATGCTCCAAACATTTTCA 435  
Qy 448 AGAGACACTGATATGTGAAAAAGCATTTTCTTCTGATATTCGCCAGATATTCCTGATGA 507  
Db 436 AGAGACACTGATATGTGAAAAAGCATTTTCTTCTGATATTCGCCAGATATTCCTGATGA 495

Qy 508 AGTAACCTGTGTCAATTATTAATTAATTCAGGCAACATGACTTGCACCTGGAATGCTRGAA 567  
Db 496 AGTAACCTGTGTCAATTATTAATTAATTCAGGCAACATGACTTGCACCTGGAATGCTRGAA 555  
Qy 568 GCTCAGCTTACATATGACACAAAATACGTGTACATGTGAAGAATTTAAGACAGAAAGAA 627  
Db 556 GCTCAGCTTACATATGACACAAAATACGTGTACATGTGAAGAATTTAAGACAGAAAGAA 615  
Qy 628 GCAACAGTATCTCACTCAAGCTATATTAACATCTCCAGTATTCATTAACAAGGTGGCAA 687  
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Db 676 GAAGTACTGTGTGGTCCAGCAGCAACGCACTAGCAGTGAAGAGTCAAAACAACACT 735  
Qy 748 GCAAAATCACCTGGATGATATATGATACCTTCTGACGCCGTCACTTTCAGAGGCTGAGAC 807  
Db 736 GCAAAATCACCTGGATGATATATGATACCTTCTGACGCCGTCACTTTCAGAGGCTGAGAC 795  
Qy 808 TATTAATGCTACAGTGGCCCAAGCCATAATTTATGGATATGCAACCAATTTGAAA 867  
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Qy 868 GGTTCCTGTGAATGAGATACAAAGCTACAAACAACCAACTGAAATGTTAAAGAATT 927  
Db 856 GGTTCCTGTGAATGAGATACAAAGCTACAAACAACCAACTGAAATGTTAAAGAATT 915  
Qy 928 TGACACCAATTTTACATATGTGCAACAGTCAGAAATTTCTACTTGGAGCCAAACATTAAGTA 987  
Db 916 TGACACCAATTTTACATATGTGCAACAGTCAGAAATTTCTACTTGGAGCCAAACATTAAGTA 975  
Qy 988 CGTATTTCAAGTGAAGTGTCAAGAAACAGGCAAAAGTACTGGCAGCTTGGAGTTACC 1047  
Db 976 CGTATTTCAAGTGAAGTGTCAAGAAACAGGCAAAAGTACTGGCAGCTTGGAGTTACC 1035  
Qy 1048 GTTTTTCATTAACAACCTGAAAACAGTCCCGAGTCAACATCAACAAAGCATTTCCAAACATGA 1107  
Db 1036 GTTTTTCATTAACAACCTGAAAACAGTCCCGAGTCAACATCAACAAAGCATTTCCAAACATGA 1095  
Qy 1108 CACATGGAATTTCTGGGCTAAACAGTTGCTTCATCTCTACAGGGCACTTACTTTCACAA 1167  
Db 1096 CACATGGAATTTCTGGGCTAAACAGTTGCTTCATCTCTACAGGGCACTTACTTTCACAA 1155  
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Qy 1288 GTTAAATCAAAATGGCTTTTATGAAGATATTCCTAATATGAAAAACAGCAATGTTGTGAA 1347  
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Qy 1348 AATGCTACAGAAAATATGTAACCTTATGATTAATTTCCAGTGAAGAGGTCTCTATATGT 1407  
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Db 1516 CAATACACAGTGTATATATATCTGATCTCAACACGTGATTAATAACCCCAAAATTTGAAA 1575  
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1576 TTTCTGCTGAGGAGGAGCCATCTCAGCAATTAATAAGAAATTAATCTTAACTTAACTTAA 1635  
1648 AACACAGGTTGATTCCTTAGACCTCAGGAATTAATCCAGGTTCAAAAGATCTAATTT 1707  
1636 AACACAGGTTGATTCCTTAGACCTCAGGAATTAATCCAGGTTCAAAAGATCTAATTT 1695  
1708 TGCCTTTCTGTTTCAAGTGAATTCATTAAGACACATATTTCTTGAGAAATTAAG 1767  
1696 TGCCTTTCTGTTTCAAGTGAATTCATTAAGACACATATTTCTTGAGAAATTAAG 1755  
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1888 TCCCTGATGAATTTGCTCTGTTTGGGAGATCGTAATGAGAGATTGCGCATCTAATTAAC 1947  
1876 TCCCTGATGAATTTGCTCTGTTTGGGAGATCGTAATGAGAGATTGCGCATCTAATTAAC 1935  
1948 TTAATTTTCCACAAAATATTTTGAAGAGCCATTCATAGGATTTCACTTTGAGAAAGTA 2007  
1936 TTAATTTTCCACAAAATATTTTGAAGAGCCATTCATAGGATTTCACTTTGAGAAAGTA 1995  
2008 GAGCTGTGTGTCAAAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2067  
1996 GAGCTGTGTGTCAAAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2055  
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2056 CTGCAATAGAAATTAAGATTCGCTCTTTTGAAGAAATTAATTAATTAATTAATTAAT 2115  
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2116 ACATGACACATGTTTCAATTTCCCTTGAGATTAATACCTAGAGAGAGAGAGAGAGAG 2175  
2188 TATGATTAAGCATATGTTTCAATTTCCCTTGAGATTAATACCTAGAGAGAGAGAGAGAG 2247  
2176 TATGATTAAGCATATGTTTCAATTTCCCTTGAGATTAATACCTAGAGAGAGAGAGAGAG 2235  
2248 CTCTACATATCAGCATATTAAGATTCGCGGAGCTCAGATGCTTTTAAATTAAGCATT 2307  
2236 CTCTACATATCAGCATATTAAGATTCGCGGAGCTCAGATGCTTTTAAATTAAGCATT 2295  
2308 CTCTGCTTAAATTTCTTAAATTAAGATTAAGATTCGCGGAGCTCAGATGCTTTTAA 2367  
2296 CTCTGCTTAAATTTCTTAAATTAAGATTAAGATTCGCGGAGCTCAGATGCTTTTAA 2355  
2368 GTCCACATATCAGCATATTAAGATTCGCGGAGCTCAGATGCTTTTAAATTAAGCAT 2427  
2356 GTCCACATATCAGCATATTAAGATTCGCGGAGCTCAGATGCTTTTAAATTAAGCAT 2415  
2428 CAATATATTTCTCTTAAATTTCTCTCAATTAAGATTAAGATTCGCGGAGCTCAGAT 2487  
2416 CAATATATTTCTCTTAAATTTCTCTCAATTAAGATTAAGATTCGCGGAGCTCAGAT 2475  
2488 AGAAGAGGATTAATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 2547  
2476 AGAAGAGGATTAATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 2535  
2548 AAAATAGATTAATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 2607  
2536 AAAATAGATTAATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 2595  
2608 CTGAGTGTGTGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 2667  
2596 CTGAGTGTGTGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 2655  
2668 ACCCTGTCTTAAATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 2727

2656 ACCCTGTCTTAAATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 2715  
2728 CAGCTACTTGTGAGAGCTGAGAGAGAGAGATTAAGATTAAGATTAAGATTAAGATTA 2787  
2716 CAGCTACTTGTGAGAGCTGAGAGAGAGAGATTAAGATTAAGATTAAGATTAAGATTA 2775  
2788 GAGCTGATTAATTTGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 2842  
2776 GAGCTGATTAATTTGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 2830

RESULT 8  
US-10-105-930-5  
; Sequence 5, Application US/10105930  
; Publication No. US20030009018A1  
; GENERAL INFORMATION:  
; APPLICANT: Meade, Meateanu  
; APPLICANT: Yaguchi, No. US20030009018A1ko  
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12  
; FILE REFERENCE: 06501-105U81  
; CURRENT FILING DATE: US/10/105,930  
; PRIOR FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER: PCT/JP00/06654  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: JP 2000-240397  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: JP 11-273358  
; NUMBER OF SEQ. ID NOS: 77  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 2123  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (98) ... (1984)  
; US-10-105-930-5

Query Match 72.8%; Score 2081.4; DB 6; Length 2123;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 2081; Conservative 2; Mismatches 8; Indels 0; Gaps 0;  
28 CAGCCAAACAAGGCTGAGAGCTGCTCTGAGAGAGATTAAGATTAAGATTAAGATTAAG 87  
7 CAGCCAAACAAGGCTGAGAGCTGCTCTGAGAGAGATTAAGATTAAGATTAAGATTAAG 66  
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67 AGAGGAAACAAGCTTTTCTGCTTCCAGACATGAATCAAGTCAATTTCAATGAGATGC 126  
148 AGTAATAGGCTTTTCAATCTTCAAGCTGAGAGAGATTAAGATTAAGATTAAGATTAAG 207  
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367 AATCTTTGGAAGCAGCATGCTTCTATGTAAGTCACTGCTGAATGTCCTCAAACTTTTCA 426  
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Db 427 AGAGACAGTATATGTGAAAAAGACATTTCTTCTGATATCCGACAGATATTCCTGATGA 486
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Db 487 AGTAACCTGATGCTATTTATGAAATTCAGGCAACATGACCTTGACCTGAAATGCTGGAA 546
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Qy 688 GAAGTATCTGGTTGGGTTCCAGAGAGAAAGCACTGAGGAGTGAAGAGTCAAAACACT 747
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Qy 1108 CACATGGAATTTCTGGGCTAACAGTGTCTCATCTCTACAGGGGACCTTACTTCTGACAA 1167
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Db 1147 CAGAGAGACATTTGATTTATTTGGGAATGATGCTTTGCTGTATGTTGTCAATTCCT 1206
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Db 1387 TGATCCCATATTTACAGAGATTAAGAAATCTTCAATCCGAAACAGAGCTCAAGCTA 1446
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Db 1447 CAAGAAGAGAAATACAGAGCCCTGAGAGACAGAGCTACCCGCAAAATCGCTATTCGA 1506
Qy 1528 CAATACTACAGTGTATATATTTCTGATCTCAACAGTGAATATTAACCCCAATTTCAA 1587
Db 1507 CAATACTACAGTGTATATATTTCTGATCTCAACAGTGAATATTAACCCCAATTTCAA 1566

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Qy 1588 TTTTCTGCTGAGGAGAGCCATCTCAGCAATTAATGAATTAATCTTCTTAACACTTAA 1647
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Qy 1648 ACCACAGTGTATCTTCTTACAGTCAAGAAATTAATCCAGGTTACAAAGACATCTTAATTT 1707
Db 1627 ACCACAGTGTATCTTCTTACAGTCAAGAAATTAATCCAGGTTACAAAGACATCTTAATTT 1686
Qy 1708 TGGTTTTTCTGTTTCAAGGTGAATTCATCAACCAACAAATTTCTTGGAGAAATTAAG 1767
Db 1687 TGGTTTTTCTGTTTCAAGGTGAATTCATCAACCAACAAATTTCTTGGAGAAATTAAG 1746
Qy 1768 CCTCATATTAATCAAGAGAAATGACAGTTCCTCTGACATACAAAACTCAGTAGAGAGAGA 1827
Db 1747 CCTCATATTAATCAAGAGAAATGACAGTTCCTCTGACATACAAAACTCAGTAGAGAGAGA 1806
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Db 1807 AACCCACATGCTTTTGGAAAAATGATTCACCAGTGAATCTATTCAGAACAGACCTGCT 1866
Qy 1888 TCCTGATGAATTTGCTCTCTGTTTGGGAGATGAGAAATGAGAGTGCATCTATTAATAC 1947
Db 1867 TCCTGATGAATTTGCTCTCTGTTTGGGAGATGAGAAATGAGAGTGCATCTATTAATAC 1926
Qy 1948 TTAATTTTCCAAATATTTTGGAAAGCCACTTCAATAGGATTTCACTTGGAAAAAGTA 2007
Db 1927 TTAATTTTCCAAATATTTTGGAAAGCCACTTCAATAGGATTTCACTTGGAAAAAGTA 1986
Qy 2008 GAGCTGTGTGTCAAAATCAATATGAGAAAGTGCCTTGAATCTGAATCTTGGGTTTTCC 2067
Db 1987 GAGCTGTGTGTCAAAATCAATATGAGAAAGTGCCTTGAATCTGAATCTTGGGTTTTCC 2046
Qy 2068 CTGCAATAGAAATTTGAATTTGCTCTTTTGGAAAAAAAGTATTCACATACAA 2122
Db 2047 CTGCAATAGAAATTTGAATTTGCTCTTTTGGAAAAAAAGTATTCACATACCA 2101

RESULT 9
US-10-105-930-9
; Sequence 9, Application US/10105930
; Publication No. US2003009018A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masaru
; APPLICANT: Yasuuchi, No. US2003009018A1ko
; TITLE OF INVENTION: NOVEL HEMOPHILIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105US1
; CURRENT APPLICATION NUMBER: US/10/105,930
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: PCT/JP00/06654
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: JP 2000-240397
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP 11-273358
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1910
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1887)
US-10-105-930-9

Query Match 66.7%; Score 1906; DB 6; Length 1910;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1906; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 119 ATGAATCAGTCACTATTCATATGAGATGCAATATTAATGCTTCTTACATCTTCACTG 178
Db 1 ATGAATCAGTCACTATTCATATGAGATGCAATATTAATGCTTCTTACATCTTCACTG 60

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179 TGTGATGAGGAATTA CAAATATATAA CTGCTGCGCCACATCTGGGTAGAACAGCCACA 238  
61 TGTGATGAGGAATTA CAAATATATAA CTGCTGCGCCACATCTGGGTAGAACAGCCACA 120  
239 ATTTTAAATGAGGTATGAAATATCTCTATATATTTCCAGACAGCATTTAAGAACTGCCAA 238  
121 ATTTTAAATGAGGTATGAAATATCTCTATATATTTCCAGACAGCATTTAAGAACTGCCAA 180  
299 CCAAGGAACTTCAATTTTATAAATAATGATCAAGAAAGATTTCAATCAACAAGATT 358  
181 CCAAGGAACTTCAATTTTATAAATAATGATCAAGAAAGATTTCAATCAACAAGATT 240  
359 AATATAACAACAGCTCGGCTTTGGTATATAAATCTTTCTGGAACCAATGCTTCTATGTAC 418  
241 AATATAACAACAGCTCGGCTTTGGTATATAAATCTTTCTGGAACCAATGCTTCTATGTAC 300  
419 TGCATCTGTAATATGTCCTCAACATTTTCAAGACACTGATATGTGAAAAAGACATTTCT 478  
301 TGCATCTGTAATATGTCCTCAACATTTTCAAGACACTGATATGTGAAAAAGACATTTCT 360  
479 TCTGATATCCGACAGATATTTCTGATGAGTAACCTGTGCTCATTTATATGATTCAGGC 538  
361 TCTGATATCCGACAGATATTTCTGATGAGTAACCTGTGCTCATTTATGAAATATTCAGGC 420  
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541 ATCTCCACTGATTCATTAACAAGGTGGCAAGAACTGTGTTGGGTCCAAAGAGCAAAAC 600  
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1019 AAAAGGACTGAGAGCTTGGAGTCA CCGTTTTCATATAAA CACCTGAAAACAGTTCCC 1078  
901 AAAAGGACTGAGAGCTTGGAGTCA CCGTTTTCATATAAA CACCTGAAAACAGTTCCC 960  
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1021 ATCTCTACAGGGACCTTACTTCTGACACACAGAGAGACATTTGACTTTTATTTGGGAATG 1080  
1199 ATGCTCTTGTCTGTATGTTGTAATCTTCTTTGATTTGGGATTTATTAACAGATCTTC 1258  
1081 ATGCTCTTGTCTGTATGTTGTAATCTTCTTTGATTTGGGATTTATTAACAGATCTTC 1140

1259 CGAATGGGATTTAAAGAAAGATCTTATGTTATATCAAAAGTGGCTTTATGAAATATTT 1318  
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1261 AATATTTCCAGTGAAGAGGTCTTATATGTTGATCCCATGATTTACAGAGATTAAGAAATC 1320  
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1321 TTCAATCCAGAACACAAAGCTTACAGACTACAGAGAGAGAAATACAGACCCCTGAGACA 1380  
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1681 CTTGACATCAAAACCTCAGTGAAGAGAGAAACCAACATCTTTTGGAAAAATGATTCACCC 1740  
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1741 AGTGAACCTATTTCCAGAACAGACCCGCTTCTGATGAAATTTGTCTCTGTTTGGGGATC 1800  
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1979 TTCAATGAGATTTCACTTTGGAAGAAATGAGAGCTGTGTGTCAAATTC 2028  
1861 TTCAATGAGATTTCACTTTGGAAGAAATGAGAGCTGTGTGTCAAATTC 1910

RESULT 10  
US-09-972-708-20  
; Sequence 20, Application US/09972708  
; Publication No. US20030059871A1  
; GENERAL INFORMATION:  
; APPLICANT: Immunex Corporation  
; APPLICANT: Cosman, David J.  
; APPLICANT: Mosley, Bruce A.  
; APPLICANT: Bird, Timothy A.  
; APPLICANT: Dubose, Robert F.  
; APPLICANT: Wiley, Steven R.  
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPR1 AND HPR2  
; FILE REFERENCE: 3160-B  
; CURRENT APPLICATION NUMBER: US/09/972, 708  
; CURRENT FILING DATE: 2001-10-05  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 1890  
; TYPE: DNA



; APPLICANT: Wiley, Steven R.  
 ; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2  
 ; FILE REFERENCE: 3160-B  
 ; CURRENT APPLICATION NUMBER: US/10/715,667  
 ; CURRENT FILING DATE: 2003-11-14  
 ; PRIOR APPLICATION NUMBER: US/09/972,708  
 ; PRIOR FILING DATE: 2001-10-05  
 ; NUMBER OF SEQ ID NOS: 29  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 20  
 ; LENGTH: 1890  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-715-667-20

Query Match 66.1%; Score 1887.6; DB 8; Length 1890;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1887; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 119 ATGAATCAGTCACTATTCATAGGATGAGTAATAGCCCTTTACATCTTCAAGCTGG 178  
 DB 1 ATGAATCAGTCACTATTCATAGGATGAGTAATAGCCCTTTACATCTTCAAGCTGG 60  
 QY 179 TGTGATGAGAGATTAACAAATATTAATGCTGCTGGCCACATCTGGGTAAACGACGACA 238  
 DB 61 TGTGATGAGAGATTAACAAATATTAATGCTGCTGGCCACATCTGGGTAAACGACGACA 120  
 QY 239 ATTTTATAGAGGTATGATATCTCTATATTTGCGACAGACAAATTAAGAACTGCCAA 298  
 DB 121 ATTTTATAGAGGTATGATATCTCTATATTTGCGACAGACAAATTAAGAACTGCCAA 180  
 QY 299 CCAAGGAACTCTATTTTATATAAATGCGATCAAGAAAGATTTCAATCAAGAGATT 358  
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 DB 301 TGCACCTGTAATGTCCCAAAACATTTCAAGAGACATGATATGTGAAAAGACATTTCT 360  
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 DB 361 TGTGATATCCGCAAGATATCTGATGAAGTAACCTGTGCAATTAATGAATATTCAGGC 420  
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 DB 421 AACAATGCTGACCTGGAATGTCTGGAAGCTCACTTAATAGACAAATATACGTGTA 480  
 QY 599 CATGTGAAGATTAGAGACAGAAAGACAAACAGTATCTCACTCAAGCTATATTAAC 658  
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 QY 659 ATCTCCACTGATTCATTACAGGTGGCAAGAGTACTTGTGGTCCAAAGACAAAC 718  
 DB 541 ATCTCCACTGATTCATTACAGGTGGCAAGAGTACTTGTGGTCCAAAGACAAAC 600  
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 DB 601 GCCTGAGGATGAAAGTCAAAACATGCAAACTTCACTGATGATATAGTAACTCT 660  
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 DB 661 TCTGACGCGTCAATTTCCAGGGCTGAGACTATAAATGCTACAGTCCCAAGACCAATATT 720  
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DB 781 ACAACCAACTTGGATGTTAAAGATTGACCAATTTTACATATGTGCAACAGTCA 840  
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 DB 1261 AATTAATCCAGTGAAGGCTCTTATATGTTGATCCCATATTAACAGATTAAGAAATC 1320  
 QY 1439 TTCAATCCAGAAACAAAGCCTTACAGACTACAAAGAGAAATACAGACCCCTGAGACA 1498  
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 QY 1559 AACACTGATATTAACCCCAATTTTCAATTTTCTGCTGAGGAAAGCCATCTCACCAAT 1618  
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 DB 1561 AATCCAGGTTACAAAGCATCTTAAATTTTCTTTTCTGTTTCAAGTGAATTCATTA 1620  
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 DB 1861 TTCAATGATTTCACTCTTGAAGAAATG 1890





Db 1549 AGGAACTATTCAGAAACAGACCCTGCTCCGATGATGATATTCCTCTGTTGGGATC 1608  
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Db 1609 GTGAATGAGAGTTGCGATCATTTATTAATCTTATTTTCCAAATATTTTGGAAAGCAC 1668  
Qy 1979 TTCAATGAGATTTCACTCTTTGAAAAAGTAG 2008  
Db 1669 TTCAATGAGATTTCACTCTTTGAAAAAGTAG 1698

## RESULT 13

US-10-715-667-22  
Sequence 22, Application US/10715667  
Publication No. US20040152161A1  
GENERAL INFORMATION:  
APPLICANT: Immunex Corporation  
APPLICANT: Cosman, David J.  
APPLICANT: Mosley, Bruce A.  
APPLICANT: Bird, Timothy A.  
APPLICANT: DuBose, Robert F.  
APPLICANT: Wiley, Steven R.  
TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2  
FILE REFERENCE: 3160-B  
CURRENT APPLICATION NUMBER: US/10/715,667  
CURRENT FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: US/09/972,708  
PRIOR FILING DATE: 2001-10-05  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 22  
LENGTH: 1698  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-715-667-22

Query Match 52.3%; Score 1493.6; DB 8; Length 1698;  
Best Local Similarity 89.7%; Pred. No. 0;  
Matches 1699; Conservative 2; Mismatches 1; Indels 192; Gaps 1;

Qy 119 ATGATCACTCACTCACTATTCATGAGATGACGTAATAGCCCTTTACATCTCTTCAAGTGG 178  
Db 1 ATGAATCAGGCTCACTATTCATGAGATGACGTAATAGCCCTTTACATCTCTTCAAGTGG 60  
Qy 179 TGTGATGAGAGATTAACAATATTAATGCTGCTGGCCACATCTGGGTGAACAGCCACA 238  
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Qy 419 TGCATGCTGAATGTCCTCAAAATTTTCAAGACACATGATATGAAAAAGACATTTCT 478  
Db 301 TGCATGCTGAATGTCCTCAAAATTTTCAAGACACATGATATGAAAAAGACATTTCT 360  
Qy 479 TCTGATATCCGCGACATATCTGATGAAGTAACCTGTCTATTATGAATATTCAGGC 538  
Db 361 TCTGATATCCGCGACATATCTGATGAAGTAACCTGTCTATTATGAATATTCAGGC 420  
Qy 539 AATGATCTGACCTGGAATGCTGGAAGCTGACCTCAATAGACAAATATCGTGTA 598  
Db 421 AATGATCTGACCTGGAATGCTGGAAGCTGACCTCAATAGACAAATATCGTGTA 480

Qy 599 CATGGAAGATTTAGACACAGAAAGAGCAACAGTATCTCACTCCAGCTATATTAAC 658  
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Qy 659 ATCTCACTGATTCATTAACAAGTGGCAAGAGTACTTGGTTGGTCCAGCAGCAAC 718  
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Qy 839 TATTTGGATATGCAACCAATTAAGAGTTTCTGTGAATGAGATTAAGGCTACA 898  
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Db 841 GAACTTCACTGAGCCAAACATTAAGTACGTAATTTCAAGTGAATGTCACAGAC 900  
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Qy 1139 ATCTACAGGACCTTACTCTGACAAACAGAGACACTTGGACTTTATTTGGAAATG 1198  
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Db 1009 CTTAATATGAAAACAGCAATGTTGAAAATGCTACAGGAAATATGTAATGAAAT 1068  
Qy 1379 AATPATTCCAGTGAAGAGGCTTATATGTTGATCCCATGATTAACAAGATTAAGAAATC 1438  
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Db 1429 AGAACAATATTTCTTGAAGATTAAGCTCATATTAATCAAGAGAAATGAGTTCT 1488  
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Qy 1859 AGTGAATCTATTCAGAGACAGACCTGCTTCTGATGAATTTGTCTCTGTTGGGATC 1918  
Db 1549 AGTGAATCTATTCAGAGACAGACCTGCTTCTGATGAATTTGTCTCTGTTGGGATC 1608  
Qy 1919 GTGAATGAGAGTTGCCATCTATTAATCTATTTTCCAAATATTTTGAAGAGCAC 1978  
Db 1609 GTGAATGAGAGTTGCCATCTATTAATCTATTTTCCAAATATTTTGAAGAGCAC 1668  
Qy 1979 TTCAATGATTTCACTCTTGAAGAGTAG 2008  
Db 1669 TTCAATGATTTCACTCTTGAAGAGTAG 1698  
RESULT 14  
US-10-105-930-3  
; Sequence 3, Application US/10105930  
; Publication No. US2003009018A1  
; GENERAL INFORMATION:  
; APPLICANT: Maeda, Masatatsu  
; TITLE OF INVENTION: NOVEL HEMOPROTEIN RECEPTOR PROTEIN, NR12  
; FILE REFERENCE: 06501-105U1  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER: PCT/JP00/06654  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: JP 2000-240397  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: JP 11-273358  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1479  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (98) ... (1381)  
US-10-105-930-3  
Query Match 46.3%; Score 1322.8; DB 6; Length 1479;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1324; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
Qy 28 CAGCCACAAGGGTGGAGGCTGCTGTGAAGTGAATTAATGCTTCAACAGGTTGAA 87  
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Qy 88 AGAGGAGAAAGCTTTTCTGCTTCAGACATGAATCACTATTCATATGAGATGC 147  
Db 67 AGAGGAGAAAGCTTTTCTGCTTCAGACATGAATCACTATTCATATGAGATGC 126  
Qy 148 AGTAATAGCCCTTACATCTCTTCACTGCTGATGATGAGAAATTAACAATTAATG 207  
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US-10-105-930-7

/ Sequence 7, Application US/10105930

/ Publication No. US2003009018A1

/ GENERAL INFORMATION:

/ APPLICANT: Maeda, Masatsugu

/ APPLICANT: Yaguchi, No. US2003009018A1ko

/ TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12

/ FILE REFERENCE: 06501-105US1

/ CURRENT APPLICATION NUMBER: US/10/105,930

/ CURRENT FILING DATE: 2002-03-25

/ PRIOR APPLICATION NUMBER: PCT/JP00/06654

/ PRIOR FILING DATE: 2000-09-27

/ PRIOR APPLICATION NUMBER: JP 2000-240397

/ PRIOR FILING DATE: 2000-08-03

/ PRIOR APPLICATION NUMBER: JP 11-273358

/ PRIOR FILING DATE: 1999-09-27

/ NUMBER OF SEQ ID NOS: 77

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 7

/ LENGTH: 1301

/ TYPE: DNA

/ ORGANISM: Homo sapiens

/ FEATURES:

/ NAME/KEY: CDS

/ LOCATION: (1)...(1284)

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## ORIGIN

Query Match 100.0%; Score 2857.4; DB 2; Length 2859;  
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 DB 61 GGAATTAATGTGCTTCAACACAGGTTGAAAGAGGAAAACAGCTTTTCTGCTTCAACAT 120  
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 DB 121 GAATCAAGTCACTATTCAATGGAGTGCATATAGCCCTTATACACTCTTCAGTGGTG 180  
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RESULT 3  
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DEFINITION Sequence 1 from patent US 6756481.  
ACCESSION AR561607  
VERSION AR561607.1 GI:53974707  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2859)  
AUTHORS Chirica, M., Kaelelein, R.A., Moore, K.W. and Parham, C.L.  
TITLE IL-23 receptor binding compositions  
JOURNAL Patent: US 6756481-A 1 29-JUN-2004;  
Schering Corporation; Kenilworth, NJ  
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LOCUS	AX338549	2859 bp	DNA	linear	PAT 09-JAN-2002
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VERSION	AX338549.1	GI:18128949			
KEYWORDS					
ORGANISM	unidentified				
SOURCE	unidentified				
REFERENCE	unclassified sequences.				
AUTHORS	1				
TITLE	Chirica, M., Kaelelein, R.A., Moore, K.W. and Parham, C.L.				
JOURNAL	Mammalian receptor proteins; related reagents and methods				
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	SCHERING CORPORATION (US)				
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DEFINITION AF461422  
ACCESSION AF461422 GI:21239251  
VERSION  
KEYWORDS  
SOURCE  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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Homidae; Homo.  
1 (bases 1 to 2826)  
Barham, C., Chirica, M., Timans, J., Vaisberg, E., Travis, M.,  
Cheung, U., Pflanz, S., Zhang, R., Singh, K.P., Vega, F., To, W.,  
Wagner, U., O'Farrell, A.-M., McClanahan, T., Zurawski, S., Hannum, C.,  
Gorman, D., Rennick, D.M., Kastelein, R.A., de Waal Malefyt, R. and  
Moore, K.W.  
A receptor for the heterodimeric cytokine IL-23 is composed of  
IL-12Rbeta1 and a novel cytokine receptor subunit, IL-23R  
J. Immunol. 168 (11), 5699-5708 (2002)  
2 (bases 1 to 2826)  
Barham, C., Chirica, M., Timans, J., Vaisberg, E., Travis, M.,  
Cheung, U., Pflanz, S., Zhang, R., Singh, K.P., Vega, F., To, W.,  
Wagner, U., O'Farrell, A.-M., McClanahan, T., Zurawski, S., Hannum, C.,  
Gorman, D., Rennick, D.M., Kastelein, R.A., de Waal Malefyt, R. and  
Moore, K.W.  
Direct Submission  
Submitted (19-DEC-2001) Immunology, DNAX Research, 901 California  
Ave., Palo Alto, CA 94304, USA  
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LOCUS			linear
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ACCESSION			BD013243.1
VERSION			BD013243.1
KEYWORDS			WO 0123556-A/3.
SOURCE			Homo sapiens (human)
ORGANISM			Homo sapiens
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AUTHORS			1 (bases 1 to 2123)
TITLE			Maeda, M. and Yaguchi, N.
			Novel hemopoietin receptor protein, NR12

JOURNAL	Patent: WO 0123556-A 3 05-Apr-2001; CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE INC., ASATSUGU MABDA, NORIKO YAGUCHI OS Homo sapiens (human) PN WO 0123556-A/3 PD 05-APR-2001 PF 27-SEP-2000 WO 2000JP06654 PR 27-SEP-1999 JP 99P 273358, 03-AUG-2000 JP 00P 240397 PI MASATSUGU MABDA, NORIKO YAGUCHI PC C12N15/12, C12N1/21, C12N5/10, C07K14/715, C07K16/28, C12P21/02, PC G01N33/567			
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 REFERENCE 1 (bases 1 to 1910)  
 AUTHORS Maeda,M. and Yaguchi,N.  
 TITLE Novel hemopoietin receptor protein, NR12  
 JOURNAL Patent: WO 0123556-A 5 05-APR-2001;  
 CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE INC, ASATSUGU MAEDA, NORIKO YAGUCHI  
 COMMENT OS Homo sapiens (human)  
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 PR 27-SEP-2000 WO 2000JP006654  
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Homidae; Homo.  
REFERENCE  
1 Cosman, D.J., Mosley, B.A., Bird, T.A., Dubose, R.F. and Wiley, S.R.  
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RESULT 10  
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 ACCESSION  
 AY937250  
 VERSION  
 AY937250.1 GI:62870698  
 KEYWORDS  
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 ORGANISM  
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 1 (bases 1 to 1779)  
 Zhang,X.Y., Zhang,H.J., Zhang,Y., Fu,Y.J., He,J., Zhu,L.P.,  
 Wang,S.H. and Liu,L.  
 Identification and expression analysis of alternatively spliced  
 isoforms of human interleukin-23 receptor gene in normal lymphoid  
 cells and selected tumor cells

JOURNAL Immunogenetics 57 (12), 934-943 (2006)  
PUBMED 16372191  
REFERENCE 2 (bases 1 to 1779)  
AUTHORS Zhang, X.-Y., Zhang, Y., Wang, S.-H. and Liu, L.  
TITLE Direct Submission  
JOURNAL Submitted (16-FEB-2005) Microbiology and Etiology, Peking Union  
Medical College, #5 Dong Dan San Tiao, Beijing 100005, China  
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LOCUS Homo sapiens interleukin 23 receptor isoform 3 fl mRNA, partial  
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ACCESSION AY937253  
VERSION AY937253.1 GI:62870704  
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Homidae; Homo.  
REFERENCE 1 (bases 1 to 1676)  
AUTHORS Zhang, X.Y., Zhang, Y., Zhang, H.-J., Fu, Y.J., He, J., Zhu, L.P.,  
Wang, S.H. and Liu, L.  
TITLE Identification and expression analysis of alternatively spliced  
isoforms of human interleukin-23 receptor gene in normal lymphoid  
cells and selected tumor cells  
JOURNAL Immunogenetics 57 (12), 934-943 (2006)  
PUBMED 16372191  
REFERENCE 2 (bases 1 to 1676)  
AUTHORS Zhang, X.-Y., Zhang, Y., Zhang, H.-J., Wang, S.-H. and Liu, L.  
TITLE Direct Submision  
JOURNAL Submitted (16-FEB-2005) Microbiology and Etiology, Peking Union  
Medical College, #5 Dong Dan San Tiao, Beijing 100005, China  
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AL389925 122289 bp DNA linear PRI 18-MAY-2005

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DEFINITION
Human DNA sequence from clone RP11-131015 on chromosome 1. Contains
the 3' end of the gene for interleukin-23 receptor (IL23R), a DNAJ
(Hsp40) homolog subfamily B member 6 (DNABJ6) pseudogene and the 5'
end of the gene for interleukin 12 receptor, beta 2 (IL12RB2),
complete sequence.
ACCESSION
AL389925 AC026054
VERSION
AL389925.10 GI:11990046
KEYWORDS
HTG; DNABJ6; IL12RB2; IL23R.
SOURCE
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ORGANISM
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 122289)
REFERENCE
Hall, R.
Direct Submission
Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk
Clone requests: clonerequests@sanger.ac.uk
On or before Nov 12, 2004 this sequence version replaced
GI:9309523, GI:11342817.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Emi; EMBL; Swi; SWISSPROT; Tr; TREMBL; Wp; WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr1
RP11-131015 is from the library RPCT-11.1 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
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Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: vegas@sanger.ac.uk
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Draft Sequence Produced by Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
http://genome.wustl.edu/gsc/index.shtml
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
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DEFINITION Sequence 22 from Patent WO0229060.  
ACCESSION AX467352  
VERSION AX467352.1 GI:21900588  
KEYWORDS  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE  
1 Cosman, D.J., Mosley, B.A., Bird, T.A., Dubose, R.F. and Wiley, S.R.  
AUTHORS Hematopoietic receptors hprt1 and hprt2  
TITLE Patent: WO 0229060-A 22 11-APR-2002;  
JOURNAL Immunex Corporation (US)  
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DEFINITION
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c8a, alternatively spliced.
ACCESSION
AY937251
VERSION
AY937251.1 GI:62870700
KEYWORDS
SOURCE
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 1618)
Zhang,X.Y., Zhang,H.J., Zhang,Y., Fu,Y.J., He,J., Zhu,L.P.,
Wang,S.H. and Liu,L.
Identification and expression analysis of alternatively spliced
isoforms of human interleukin-23 receptor gene in normal lymphoid
cells and selected tumor cells
Immunogenetics 57 (12), 934-943 (2006)
16372191
2 (bases 1 to 1618)
Zhang,X.-Y., Zhang,Y., Wang,S.-H. and Liu,L.
Direct Submission
Submitted (16-FEB-2005) Microbiology and Etiology, Peking Union
Medical College, #5 Dong Dan San Tiao, Beijing 100005, China
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 DB 1280 GACTCAGAAATTAATCCAGGTATCAAAAGCATCTTAATTTGCTTTTCTGTTCAAGT 1339

QY 1727 GTGAATTCATTAAGCAACATATTTCTTGAAGAAATTAAGCTCATTAATTAATCAAGA 1786  
 DB 1340 GTGAATTCATTAAGCAACATATTTCTTGAAGAAATTAAGCTCATTAATTAATCAAGA 1399

QY 1787 GAATGAGTTCTCTGACATACAAACCTAGTGAAGAGAAACCAATGCTTTTGAA 1846  
 DB 1400 GAATGAGTTCTCTGACATACAAACCTAGTGAAGAGAAACCAATGCTTTTGAA 1459

QY 1847 AATGATTCACCCAGTGAATCTATTTCCAGAACAGACCTGCTTCTGATGAATTTGTCTCC 1906  
 DB 1460 AATGATTCACCCAGTGAATCTATTTCCAGAACAGACCTGCTTCTGATGAATTTGTCTCC 1519

QY 1907 TGTTTGGGATCGTGAATGAGAGTGGCCATCTATTAATCTTATTTTCCACAAATATTT 1966  
 DB 1520 TGTTTGGGATCGTGAATGAGAGTGGCCATCTATTAATCTTATTTTCCACAAATATTT 1579

QY 1967 TTGAAAGCCACTTCAATAGGATTTCACTCTTGAAAAAG 2005  
 DB 1580 TTGAAAGCCACTTCAATAGGATTTCACTCTTGAAAAAG 1618

Search completed: October 14, 2006, 17:19:15  
 Job time : 15919 secs



GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: October 14, 2006, 13:44:26 : Search time 566 Seconds  
(without alignments)  
9438.089 Million cell updates/sec

Title: US-10-667-289-1

Perfect score: 2857.4

Sequence: 1 ggtgacgggaattccatctg.....gtctggaataaaaaaaaaa 2859

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2395520 seqs, 934235491 residues

Total number of hits satisfying chosen parameters: 4791040

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA.New:\*  
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2: /EMC\_Celerra\_SIDS3/Prodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
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9: /EMC\_Celerra\_SIDS3/Prodata/1/pubpna/US11\_NEW\_PUB.seq3:\*  
10: /EMC\_Celerra\_SIDS3/Prodata/1/pubpna/US60\_NEW\_PUB.seq2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2081.4	72.8	2123	8	US-11-274-375-5
2	1906	66.7	1910	8	US-11-274-375-9
3	1322.8	46.3	1479	8	US-11-274-375-3
4	1236.6	43.3	1301	8	US-11-274-375-7
5	1039.2	36.4	1784	8	US-11-274-375-1
6	254	8.9	36871	6	US-10-539-228-682
7	248.6	8.7	44567	7	US-11-330-648-46
8	247	8.6	81001	7	US-11-412-373-1
9	246.8	8.6	438732	6	US-10-669-920-341
10	245.4	8.6	1000	8	US-11-266-748A-292995
11	245.4	8.6	1000	8	US-11-266-748A-344424
12	245.4	8.6	1000	8	US-11-266-748A-404879
13	245.4	8.6	1000	8	US-11-266-748A-475925
14	244.8	8.6	225587	6	US-10-540-898-374
15	244.4	8.6	84105	6	US-10-669-920-1403
16	244.4	8.5	44423	9	US-11-035-114-1
17	244.2	8.5	48600	8	US-11-266-748A-25014
18	244.2	8.5	420555	6	US-10-669-920-1140
19	244.2	8.5	420555	6	US-10-669-920-1151
20	242.6	8.5	1000	8	US-11-266-748A-201057
21	242.6	8.5	1000	8	US-11-266-748A-205385
22	242.6	8.5	113196	8	US-11-266-748A-59091
23	242.6	8.5	203010	8	US-11-266-748A-59417

C 24	242.2	8.5	127145	8	US-11-266-748A-59222	Sequence 59222, A
C 25	242.2	8.5	227246	6	US-10-539-228-314	Sequence 314, App
C 26	241.2	8.4	142281	6	US-11-266-748A-23957	Sequence 23957, A
C 27	241	8.4	49355	6	US-10-540-898-787	Sequence 787, App
C 28	240.8	8.4	1000	8	US-11-266-748A-114953	Sequence 114953, A
C 29	240.8	8.4	1000	8	US-11-266-748A-120084	Sequence 120084, A
C 30	240.8	8.4	1000	8	US-11-266-748A-280673	Sequence 280673, A
C 31	240.8	8.4	1000	8	US-11-266-748A-282815	Sequence 282815, A
C 32	240.8	8.4	1000	8	US-11-266-748A-309455	Sequence 309455, A
C 33	240.8	8.4	1000	8	US-11-266-748A-392371	Sequence 392371, A
C 34	240.8	8.4	1000	8	US-11-266-748A-483089	Sequence 483089, A
C 35	240.6	8.4	1000	8	US-11-266-748A-224342	Sequence 224342, A
C 36	240.6	8.4	1000	8	US-11-266-748A-246596	Sequence 246596, A
C 37	240.6	8.4	1000	8	US-11-266-748A-293196	Sequence 293196, A
C 38	240.6	8.4	1000	8	US-11-266-748A-344625	Sequence 344625, A
C 39	240.6	8.4	1000	8	US-11-266-748A-405114	Sequence 405114, A
C 40	240.6	8.4	1000	8	US-11-266-748A-476160	Sequence 476160, A
C 41	240.6	8.4	1418	8	US-11-266-748A-31435	Sequence 31435, A
C 42	240.6	8.4	171653	8	US-11-266-748A-22660	Sequence 22660, A
C 43	240.4	8.4	4647455	6	US-10-641-321-205	Sequence 205, App
C 44	240	8.4	180237	6	US-10-539-228-308	Sequence 308, App
C 45	239.8	8.4	1000	8	US-11-266-748A-205230	Sequence 205230, A

#### ALIGNMENTS

RESULT 1  
US-11-274-375-5  
Sequence 5, Application US/11274375  
Publication No. US20060106201A1  
GENERAL INFORMATION:  
APPLICANT: Maeda, Masaen  
TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12  
FILE REFERENCE: 06501-105U81  
CURRENT APPLICATION NUMBER: US/11/274,375  
CURRENT FILING DATE: 2005-11-14  
PRIOR APPLICATION NUMBER: US/10/105,930  
PRIOR FILING DATE: 2002-03-25  
PRIOR APPLICATION NUMBER: PCT/JP00/06654  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: JP 2000-240397  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: JP 11-273358  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5  
LENGTH: 2123  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (98)...(1984)  
US-11-274-375-5

Query Match 72.8%, Score 2081.4, DB 8, Length 2123;  
Best Local Similarity 99.5%, Pred. No. 1.9e-278;  
Matches 2085; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY	28	CAGCGAAGAGGTCGAGCTGCTGCTGAGGATTAATGCTTCAAGAGTTGAA	87
DB	7	CAGCGAAGAGGTCGAGCTGCTGCTGAGGATTAATGCTTCAAGAGTTGAA	66
QY	88	AGAGGAAACAGCTTTTCTGCTTCAGACATGAATCAATGATTAATGAGATGC	147
DB	67	AGAGGAAACAGCTTTTCTGCTTCAGACATGAATCAATGATTAATGAGATGC	126
QY	148	AGTAATAGCCCTTACATCTCTTCAGCTGCTGATCATGAGAAATTAATTAATCTG	207
DB	127	AGTAATAGCCCTTACATCTCTTCAGCTGCTGATCATGAGAAATTAATTAATCTG	186

QY 208 CTCTGGCACATCTGGGTAGAACCCACCAATTTTAAAGTGGTAATGTAATCTCTAT 267  
Db 187 CTCTGGCCACATCTGGGTAGAACCCACCAATTTTAAAGTGGTGTGTAATCTCTAT 246  
QY 268 AATATGCAAGCAAGCAATTAAGAACTGGCAACCAAGAACTTCTATTTTAAATGG 327  
Db 247 AATATGCAAGCAAGCAATTAAGAACTGGCAACCAAGAACTTCTATTTTAAATGG 306  
QY 328 CATCAAGAAAGATTTCAATTCACAAAGATTAATTAACAACAGCTGGCTTGTATTA 387  
Db 307 CATCAAGAAAGATTTCAATTCACAAAGATTAATTAACAACAGCTGGCTTGTATTA 366  
QY 388 AAATCTTCTGAAACCAATCTCTATGTAAGTCACTGTAATGTCCCAACATTTTCA 447  
Db 367 AAATCTTCTGAAACCAATCTCTATGTAAGTCACTGTAATGTCCCAACATTTTCA 426  
QY 448 AGAGACCTGATATGTAAGAAAGCAATTTCTGTAATTCGGCAATATTCCTGATGA 507  
Db 427 AGAGACCTGATATGTAAGAAAGCAATTTCTGTAATTCGGCAATATTCCTGATGA 486  
QY 508 AGTAACCTGTGCAATTTATGTAATTTCAAGCAACATGTAAGTCACTGTAATGTGAA 567  
Db 487 AGTAACCTGTGCAATTTATGTAATTTCAAGCAACATGTAAGTCACTGTAATGTGAA 546  
QY 568 GCTCACTCAATAGACAAATAATGCTGTACATGTGAAGATTAGAGACAGAAAGAA 627  
Db 547 GCTCACTCAATAGACAAATAATGCTGTACATGTGAAGATTAGAGACAGAAAGAA 606  
QY 628 GCAACAGTATCTCACTCAAGCTATTAATCATCTCCAGTATTCATTAAGAGTGGCA 687  
Db 607 GCAACAGTATCTCACTCAAGCTATTAATCATCTCCAGTATTCATTAAGAGTGGCA 666  
QY 688 GAAGTACTTGGTGGTCCAAAGCAAGCAAGCACTAGGAGTGAAGATCAAAACAAT 747  
Db 667 GAAGTACTTGGTGGTCCAAAGCAAGCAAGCACTAGGAGTGAAGATCAAAACAAT 726  
QY 748 GCAATTCACCTGATATATGTAATCTTCTGACGCGTCAATTTCCAGGCGTGAAC 807  
Db 727 GCAATTCACCTGATATATGTAATCTTCTGACGCGTCAATTTCCAGGCGTGAAC 786  
QY 808 TATTAATGCTACAGTGGCCAAAGCAATTTATTTGGAATATGTAATCAACAAATTTGAAA 867  
Db 787 TATTAATGCTACAGTGGCCAAAGCAATTTATTTGGAATATGTAATCAACAAATTTGAAA 846  
QY 868 GGTTCCTGTGAATAGATACAAAGCTACAAACAACCTGTAATTTAAAGATTT 927  
Db 847 GGTTCCTGTGAATAGATACAAAGCTACAAACAACCTGTAATTTAAAGATTT 906  
QY 928 TGACACCAATTTTACATATGTGCAACAGTCAGAAATTTCTATGAGCCAAACATTAAAGTA 987  
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QY 988 CGTATTTCAAGTGAATGTCAAGAAACAGGCAAAAGTATCTGGAGCTTGGAGTTACC 1047  
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QY 1048 GTTTTTCATTAACACCTGAAACAGTTCGCCAGGTCAATCAAAAGATTTCCAAACATGA 1107  
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QY 1108 CACATGGAATTTCTGGGCTAACAGTGTCTTCATCTCAAGAGGACCTTATCTGACAA 1167  
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QY 1228 TTTCTTATTTGGATTTTAAACAGATCTCCGAATGGGATTTAAAGAAAGATCTTATTT 1287  
Db 1207 TTTCTTATTTGGATTTTAAACAGATCTCCGAATGGGATTTAAAGAAAGATCTTATTT 1266  
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Db 1267 GTTAATACCAAGTGGCTTATGAAAGATATTCCTAATATGAAAAACAGCAATGTGTGAA 1326  
QY 1348 AATGCTACAGAAATATGTAAGCTTATGTAATTAATTTCAAGTGAACAGGTCTTATATGT 1407  
Db 1327 AATGCTACAGAAATATGTAAGCTTATGTAATTAATTTCAAGTGAACAGGTCTTATATGT 1386  
QY 1408 TGATCCCATGATTTACAGAGATTAAGAAATCTTCAATCCCAAGACAAAGCTTACAGACTA 1467  
Db 1387 TGATCCCATGATTTACAGAGATTAAGAAATCTTCAATCCCAAGACAAAGCTTACAGACTA 1446  
QY 1468 CAAAGAGGAAATACAGAGACCCCTGAGACAAAGACTACCCCAAACTCCGCTATTTGGA 1527  
Db 1447 CAAAGAGGAAATACAGAGACCCCTGAGACAAAGACTACCCCAAACTCCGCTATTTGGA 1506  
QY 1528 CAATACCAAGTGTATATATTTCTGATCTCAACATGTAATTAACCCCAATTTTCAAA 1587  
Db 1507 CAATACCAAGTGTATATATTTCTGATCTCAACATGTAATTAACCCCAATTTTCAAA 1566  
QY 1588 TTTTCTGCTGAGGAAAGCCATCTCAGCAATTAATTAAGAAATTTCTTCAACTTAA 1647  
Db 1567 TTTTCTGCTGAGGAAAGCCATCTCAGTAATTAATTAAGAAATTTCTTCAACTTAA 1626  
QY 1648 ACCACAGTGTATTTCTTGAAGCTCAGAAATATATCCAGGTTACAAAGATCTTAAATTT 1707  
Db 1627 ACCACAGTGTATTTCTTGAAGCTCAGAAATATATCCAGGTTACAAAGATCTTAAATTT 1686  
QY 1708 TGCCTTTTCTGTTCAAGTGTGAATCACTAAGCAACAATATTTCTTGAAGATTTAAAG 1767  
Db 1687 TGCCTTTTCTGTTCAAGTGTGAATCACTAAGCAACAATATTTCTTGAAGATTTAAAG 1746  
QY 1768 CCTCATATTAATCAAGAGATGCAAGTCTCTGACATACAAACTCAGTAGAGAGGA 1827  
Db 1747 CCTCATATTAATCAAGAGATGCAAGTCTCTGACATACAAACTCAGTAGAGAGGA 1806  
QY 1828 AACACAGTGTGTGGAATTAATTAATTTCAAGTGAATCTATTTCCAGAAACAGACCTGTCT 1887  
Db 1807 AACACAGTGTGTGGAATTAATTAATTTCAAGTGAATCTATTTCCAGAAACAGACCTGTCT 1866  
QY 1888 TCCGTGATGAATTTGTCTCTGTTGGGGAATCGTAATGAGAGTTCATCTTAAATAC 1947  
Db 1867 TCCGTGATGAATTTGTCTCTGTTGGGGAATCGTAATGAGAGTTCATCTTAAATAC 1926  
QY 1948 TTAATTTCCAAATAATTTTGGAAAGCACTTCAATAGGATTTCACTTGGAAAAAGTA 2007  
Db 1927 TTAATTTCCAAATAATTTTGGAAAGCACTTCAATAGGATTTCACTTGGAAAAAGTA 1986  
QY 2008 GAGCTGTGTGTCAAATTAATTAAGAAAGTGCCTGCAATCTGAATCTGGGTTTCC 2067  
Db 1987 GAGCTGTGTGTCAAATTAATTAAGAAAGTGCCTGCAATCTGAATCTGGGTTTCC 2046  
QY 2068 CTGCAATAGAAATTTGAATTTGCTCTTTTGAAGAAATGTAATTCACATACAAA 2122  
Db 2047 CTGCAATAGAAATTTGAATTTGCTCTTTTGAAGAAATGTAATTCACATACAAA 2101

## RESULT 2

US-11-274-375-9

Sequence 9, Application US/11274375

Publication No. US20060106201A1

GENERAL INFORMATION:

APPLICANT: Maeda, Masatatsu

APPLICANT: Yaguchi, Noriko

TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12

FILE REFERENCE: 06501-105US1

CURRENT APPLICATION NUMBER: US/11/274, 375

PRIOR APPLICATION NUMBER: US/10/105, 930

PRIOR FILING DATE: 2002-03-25

PRIOR APPLICATION NUMBER: PCT/JP00/06654

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: JP 2000-240397

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: JP 11-273358  
PRIOR FILING DATE: 1999-09-27  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 9  
LENGTH: 1910  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(1887)  
US-11-274-375-9

Query Match 66.7%; Score 1906; DB 8; Length 1910;  
Best Local Similarity 99.8%; Pred. No. 2,6e-254;  
Matches 1906; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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1 ATGAATCAGGTCACTATTCAATGGATGCAATAGCCCTTTACATACCTTCAGCTGG 60  
179 TGTCAATGAGGATTTACAAATATTAATCTGCTGGCCCAATCTGGGTAGAACAGCCCA 238  
61 TGTCAATGAGGATTTACAAATATTAATCTGCTGGCCCAATCTGGGTAGAACAGCCCA 120  
239 ATTTTAAAGTGGATTTGAATATCTCATATATTGGCCAGCAGCAATTAAGAACTGGCAA 298  
121 ATTTTAAAGTGGATTTGAATATCTCATATATTGGCCAGCAGCAATTAAGAACTGGCAA 180  
299 CCAAGGAACTTCATTTTATTAATAATGCGATCAAGAAAGATTTCATACAGAGATT 358  
181 CCAAGGAACTTCATTTTATTAATAATGCGATCAAGAAAGATTTCATACAGAGATT 240  
359 AATPAAACACAGCTCGCTTTGGTATATAAATCTTTTGGACCAATGCTTCTATGTAC 418  
241 AATPAAACACAGCTCGCTTTGGTATATAAATCTTTTGGACCAATGCTTCTATGTAC 300  
419 TGAAGCTGAATGCTCCCAAAATTTTCAAGAGCACTGATATGTGAAAGACATTTCT 478  
301 TGAAGCTGAATGCTCCCAAAATTTTCAAGAGCACTGATATGTGAAAGACATTTCT 360  
479 TCTGATATCCGCGAGATATCTCTGATGAAGTAACCTGTGCAATTAATGAATTCAGGC 538  
361 TCTGATATCCGCGAGATATCTCTGATGAAGTAACCTGTGCAATTAATGAATTCAGGC 420  
539 AATGATCTTGCACTCTGGAATGCTGGAAGCTCACTTACATAGACAAATATCTGTGA 598  
421 AATGATCTTGCACTCTGGAATGCTGGAAGCTCACTTACATAGACAAATATCTGTGA 480  
599 CATGTGAAGTTTGAAGAGAGAAAGACCAAGATCTCACTCACTCACTATATTAAC 658  
481 CATGTGAAGTTTGAAGAGAGAGAAAGACCAAGATCTCACTCACTCACTATATTAAC 540  
659 ATCTCCACTGATTCATTAACAAGGTGCAAGAAAGTATGTTGGTCCAAAGCAAAAC 718  
541 ATCTCCACTGATTCATTAACAAGGTGCAAGAAAGTATGTTGGTCCAAAGCAAAAC 600  
719 GCACTAGGATGGAAGAGTCAAAACCACTGCAATTCACCTGATGATATATGATACCT 778  
601 GCACTAGGATGGAAGAGTCAAAACCACTGCAATTCACCTGATGATATATGATACCT 660  
779 TCTGAGCCCTGATTTCCAGGCGTGAAGCTTAAATGCTACAGTCCCAAGACCAATAT 838  
661 TCTGAGCCCTGATTTCCAGGCGTGAAGCTTAAATGCTACAGTCCCAAGACCAATAT 720  
839 TATTTGGATAGTCAAAACCAATTAAGAAAGTTCCTGTGAATGATATCAAGGCTACA 898  
721 TATTTGGATAGTCAAAACCAATTAAGAAAGTTCCTGTGAATGATATCAAGGCTACA 780  
899 ACAACCAACTTGGAAATGTTAAAGAAATTTGACCAATTTTACATATGTGCAACAGTCA 958  
781 ACAACCAACTTGGAAATGTTAAAGAAATTTGACCAATTTTACATATGTGCAACAGTCA 840

959 GAATTTACTTGGAGCCAAACATTAAAGTACGTAATTTCAAGTGAAGTCAAGAAACAGGC 1018  
841 GAATTTACTTGGAGCCAAACATTAAAGTACGTAATTTCAAGTGAAGTCAAGAAACAGGC 900  
1019 AAAAGTACTTGGAGCCCTGAGGTTCAACGTTTTCATTAACACCTGAAACAGTTCCC 1078  
901 AAAAGTACTTGGAGCCCTGAGGTTCAACGTTTTCATTAACACCTGAAACAGTTCCC 960  
1079 CAGGTCACTCAAAAGACATTCACATGACACATGAAATTCGGGCTTAAACAGTTGCTCC 1138  
961 CAGGTCACTCAAAAGACATTCACATGACACATGAAATTCGGGCTTAAACAGTTGCTCC 1020  
1139 ATCTTCAAGGACCTTACTTGAACAAGAGACATTCGACTTTTATGGGAATG 1198  
1021 ATCTTCAAGGACCTTACTTGAACAAGAGACATTCGACTTTTATGGGAATG 1080  
1199 ATGCTCTTGGCTTATGTTGTCATATCTTTCTTGAATGGATATTTAACAATCATTC 1258  
1081 ATGCTCTTGGCTTATGTTGTCATATCTTTCTTGAATGGATATTTAACAATCATTC 1140  
1259 CGAAGTGGGATTTAAAGAAAGATCTTATGTTAATACAAAGTGGCTTTATGAAGATTT 1318  
1141 CGAAGTGGGATTTAAAGAAAGATCTTATGTTAATACAAAGTGGCTTTATGAAGATTT 1200  
1319 CCTAATATGAAAAACAGCAATGTTGAAATGCTA CAGGAAATATGTAACCTTAAT 1378  
1201 CCTAATATGAAAAACAGCAATGTTGAAATGCTA CAGGAAATATGTAACCTTAAT 1260  
1379 AATPAAATGAGAGAGAGCTCTTATGTTGATCCCATGATTCACAGATTAAGAAATC 1438  
1261 AATPAAATGAGAGAGAGCTCTTATGTTGATCCCATGATTCACAGATTAAGAAATC 1320  
1439 TTCAATCCAGAAACAGAGCTTACAGCTA CAAAGAGAGATACAGGACCCCTGAGACA 1498  
1321 TTCAATCCAGAAACAGAGCTTACAGCTA CAAAGAGAGATACAGGACCCCTGAGACA 1380  
1499 AGAGACTAACCCGAAACCTGCTATTCGACATATCTACAGTTGATATATCTCTGATCTC 1558  
1381 AGAGACTAACCCGAAACCTGCTATTCGACATATCTACAGTTGATATATCTCTGATCTC 1440  
1559 AATCCTGATATTAACCCCAATTTGAAATTTCTGCTGAGGAAAGCCATCTCAGCAAT 1618  
1441 AATCCTGATATTAACCCCAATTTGAAATTTCTGCTGAGGAAAGCCATCTCAGCAAT 1500  
1619 AATPAAATTAATCTCTTAACCTTAACCTTAACCAAGAGTGTATCTTACAGCAAT 1678  
1501 AATPAAATTAATCTCTTAACCTTAACCTTAACCAAGAGTGTATCTTACAGCAAT 1560  
1679 AATCCAGGTTACAAAGACATCTTAATTTTGTCTTTTCTGTTCAAGTGAATTCACCTA 1738  
1561 AATCCAGGTTACAAAGACATCTTAATTTTGTCTTTTCTGTTCAAGTGAATTCACCTA 1620  
1739 AGCAACCAATATTTCTTGAAGATTAAGCTTCATTAATCAAGAGATCAAGTTCT 1798  
1621 AGCAACCAATATTTCTTGAAGATTAAGCTTCATTAATCAAGAGATCAAGTTCT 1680  
1799 CTTGACATCAAAACCTGATGAGAGAGAAACCAACATGCTTTTGGAAAAATGATCACCC 1858  
1681 CTTGACATCAAAACCTGATGAGAGAGAAACCAACATGCTTTTGGAAAAATGATCACCC 1740  
1859 AGTGAACATATTCAGAACAGACCTGCTTCTGATGAATTTTCTCTGTTGGGGATC 1918  
1741 AGTGAACATATTCAGAACAGACCTGCTTCTGATGAATTTTCTCTGTTGGGGATC 1800  
1919 GTGAATGAGAGTTCATCTATTAATTAATTTTCACAAAATATTTTGAAGACAC 1978  
1801 GTGAATGAGAGTTCATCTATTAATTAATTTTCACAAAATATTTTGAAGACAC 1860  
1979 TTCAATGATTTCACTCTTGGAAAGTGAAGTGTGTGCTCAAAATCA 2028  
1861 TTCAATGATTTCACTCTTGGAAAGTGAAGTGTGTGCTCAAAATCA 1910





QY 208 CTCGCGCACTCTGGGTAGAACCAAGCAATTTTAAAGATGGATATGATATCTCTAT 267  
| | | | |  
DB 187 CTCGCGCACTCTGGGTAGAACCAAGCAATTTTAAAGATGGATATGATATCTCTAT 246  
| | | | |  
QY 268 ATATTGCGAAGCGCAATTAAGATCTGCCAACAAGAACTTCAATTTTATAAAATGG 327  
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DB 247 ATATTGCGAAGCGCAATTAAGATCTGCCAACAAGAACTTCAATTTTATAAAATGG 306  
| | | | |  
QY 328 CATCAAGAAAGATTTCAATCAACAAGATTTAATAAACAAGCTCGCTTGTATTA 387  
| | | | |  
DB 307 CATCAAGAAAGATTTCAATCAACAAGATTTAATAAACAAGCTCGCTTGTATTA 366  
| | | | |  
QY 388 AAATCTTGTGAACCAATCTTGTATGATGCAAGCTGCTGAATGTCCCAATTTTCA 447  
| | | | |  
DB 367 AAATCTTGTGAACCAATCTTGTATGATGCAAGCTGCTGAATGTCCCAATTTTCA 426  
| | | | |  
QY 448 AGAGACACTGATATGAGAAAGACATTTCTGTGATATCGGCAATTCCTGATGA 507  
| | | | |  
DB 427 AGAGACACTGATATGAGAAAGACATTTCTGTGATATCGGCAATTCCTGATGA 486  
| | | | |  
QY 508 AGTAACCTGTGATTTATTAATATTCAGGCAATGATCTTGCACTGAAATCTTGAA 567  
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DB 487 AGTAACCTGTGATTTATTAATATTCAGGCAATGATCTTGCACTGAAATCTTGAG 546  
| | | | |  
QY 568 GCTCACCCTCAATAGACAAATATCGTGTACATGTGAAGATTTAGACACAGAAAGA 627  
| | | | |  
DB 547 GCTCACCCTCAATAGACAAATATCGTGTACATGTGAAGATTTAGACACAGAAAGA 606  
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QY 628 GCAACAGTATCTGACCTCAAGCTATATTAATCTCCAGATTTTCAAGGTGCA 687  
| | | | |  
DB 607 GCAACAGTATCTGACCTCAAGCTATATTAATCTCCAGATTTTCAAGGTGCA 666  
| | | | |  
QY 688 GAAGTCTGTGTTGGTCCAGACAGAAACGCACTAGCATGGAAGATCAAAACACT 747  
| | | | |  
DB 667 GAAGTCTGTGTTGGTCCAGACAGAAACGCACTAGCATGGAAGATCAAAACACT 726  
| | | | |  
QY 748 GCAATTCACCTGATATATGATATCTTGTGACGCGTCAATTTCCAGGCTGAGAC 807  
| | | | |  
DB 727 GCAATTCACCTGATATATGATATCTTGTGACGCGTCAATTTCCAGGCTGAGAC 786  
| | | | |  
QY 808 TATTAATGCTACAGTGGCCAAAGCCATTAATTTATGGGATAGTCAACCAATTA 867  
| | | | |  
DB 787 TATTAATGCTACAGTGGCCAAAGCCATTAATTTATGGGATAGTCAACCAATTA 846  
| | | | |  
QY 868 GATTTCCTGTAATGATATGATATCAAGGCTCAACAAACCTTGAATGTTAAAGATT 927  
| | | | |  
DB 847 GATTTCCTGTAATGATATGATATCAAGGCTCAACAAACCTTGAATGTTAAAGATT 906  
| | | | |  
QY 928 TGACACCAATTTTACATATGTCACAGTCAGAAATTTCTAGTGGCCAAACATTA 987  
| | | | |  
DB 907 TGACACCAATTTTACATATGTCACAGTCAGAAATTTCTAGTGGCCAAACATTA 966  
| | | | |  
QY 988 CGTATTTCAGATGATATGTCAGAAACAGGCAAAAGGTACTGACGCTTGGAGTTCA 1047  
| | | | |  
DB 967 CGTATTTCAGATGATATGTCAGAAACAGGCAAAAGGTACTGACGCTTGGAGTTCA 1026  
| | | | |  
QY 1048 GTTTTTCATAAACACCTGAAACAGTT 1075  
| | | | |  
DB 1027 GTTTTTCATAAACACCTGAAACAGTT 1054  
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RESULT 6  
US-10-539-228-682  
; Sequence 682, Application US/10539228  
; Publication No. US20060154250A1  
; GENERAL INFORMATION:  
; APPLICANT: David W. Morris  
; APPLICANT: Marc S. Malandro  
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer  
; FILE REFERENCE: CHIR0052-101 (PP023370.0003)  
; CURRENT APPLICATION NUMBER: US/10/539,228  
; PRIOR FILING DATE: 2005-06-17  
; PRIOR APPLICATION NUMBER: US 10/322,281

QY 208 CTCGCGCACTCTGGGTAGAACCAAGCAATTTTAAAGATGGATATGATATCTCTAT 267  
| | | | |  
DB 187 CTCGCGCACTCTGGGTAGAACCAAGCAATTTTAAAGATGGATATGATATCTCTAT 246  
| | | | |  
QY 268 ATATTGCGAAGCGCAATTAAGATCTGCCAACAAGAACTTCAATTTTATAAAATGG 327  
| | | | |  
DB 247 ATATTGCGAAGCGCAATTAAGATCTGCCAACAAGAACTTCAATTTTATAAAATGG 306  
| | | | |  
QY 328 CATCAAGAAAGATTTCAATCAACAAGATTTAATAAACAAGCTCGCTTGTATTA 387  
| | | | |  
DB 307 CATCAAGAAAGATTTCAATCAACAAGATTTAATAAACAAGCTCGCTTGTATTA 366  
| | | | |  
QY 388 AAATCTTGTGAACCAATCTTGTATGATGCAAGCTGCTGAATGTCCCAATTTTCA 447  
| | | | |  
DB 367 AAATCTTGTGAACCAATCTTGTATGATGCAAGCTGCTGAATGTCCCAATTTTCA 426  
| | | | |  
QY 448 AGAGACACTGATATGAGAAAGACATTTCTGTGATATCGGCAATTCCTGATGA 507  
| | | | |  
DB 427 AGAGACACTGATATGAGAAAGACATTTCTGTGATATCGGCAATTCCTGATGA 486  
| | | | |  
QY 508 AGTAACCTGTGATTTATTAATATTCAGGCAATGATCTTGCACTGAAATCTTGAA 567  
| | | | |  
DB 487 AGTAACCTGTGATTTATTAATATTCAGGCAATGATCTTGCACTGAAATCTTGAG 546  
| | | | |  
QY 568 GCTCACCCTCAATAGACAAATATCGTGTACATGTGAAGATTTAGACACAGAAAGA 627  
| | | | |  
DB 547 GCTCACCCTCAATAGACAAATATCGTGTACATGTGAAGATTTAGACACAGAAAGA 606  
| | | | |  
QY 628 GCAACAGTATCTGACCTCAAGCTATATTAATCTCCAGATTTTCAAGGTGCA 687  
| | | | |  
DB 607 GCAACAGTATCTGACCTCAAGCTATATTAATCTCCAGATTTTCAAGGTGCA 666  
| | | | |  
QY 688 GAAGTCTGTGTTGGTCCAGACAGAAACGCACTAGCATGGAAGATCAAAACACT 747  
| | | | |  
DB 667 GAAGTCTGTGTTGGTCCAGACAGAAACGCACTAGCATGGAAGATCAAAACACT 726  
| | | | |  
QY 748 GCAATTCACCTGATATATGATATCTTGTGACGCGTCAATTTCCAGGCTGAGAC 807  
| | | | |  
DB 727 GCAATTCACCTGATATATGATATCTTGTGACGCGTCAATTTCCAGGCTGAGAC 786  
| | | | |  
QY 808 TATTAATGCTACAGTGGCCAAAGCCATTAATTTATGGGATAGTCAACCAATTA 867  
| | | | |  
DB 787 TATTAATGCTACAGTGGCCAAAGCCATTAATTTATGGGATAGTCAACCAATTA 846  
| | | | |  
QY 868 GATTTCCTGTAATGATATGATATCAAGGCTCAACAAACCTTGAATGTTAAAGATT 927  
| | | | |  
DB 847 GATTTCCTGTAATGATATGATATCAAGGCTCAACAAACCTTGAATGTTAAAGATT 906  
| | | | |  
QY 928 TGACACCAATTTTACATATGTCACAGTCAGAAATTTCTAGTGGCCAAACATTA 987  
| | | | |  
DB 907 TGACACCAATTTTACATATGTCACAGTCAGAAATTTCTAGTGGCCAAACATTA 966  
| | | | |  
QY 988 CGTATTTCAGATGATATGTCAGAAACAGGCAAAAGGTACTGACGCTTGGAGTTCA 1047  
| | | | |  
DB 967 CGTATTTCAGATGATATGTCAGAAACAGGCAAAAGGTACTGACGCTTGGAGTTCA 1026  
| | | | |  
QY 1048 GTTTTTCATAAACACCTGAAACAGTT 1075  
| | | | |  
DB 1027 GTTTTTCATAAACACCTGAAACAGTT 1054  
| | | | |  
RESULT 7  
US-11-330-648-46/c  
; Sequence 46, Application US/11330648  
; Publication No. US20060211015A1  
; GENERAL INFORMATION:  
; APPLICANT: Engelhard, Eric  
; APPLICANT: Morris, David  
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER  
; FILE REFERENCE: 20366-042002  
; CURRENT APPLICATION NUMBER: US/11/330,648  
; PRIOR FILING DATE: 2006-01-12  
; PRIOR APPLICATION NUMBER: US 10/004,113  
; PRIOR FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: US 09/747,377  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 09/798,586  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 46  
; LENGTH: 44567  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-330-648-46  
Query Match 8.9%; Score 248.6; DB 7; Length 44567;  
Best Local Similarity 78.5%; Pred. No. 1.4e-26;  
Matches 296; Conservative 1; Mismatches 80; Indels 0; Gaps 0;  
QY 2483 TGTACGAAAGGATTAATATGCAAAATACCTGTGATTAATGCTGAAATTTTC 2542  
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Db      590 TGTCTCAAAAAAAAAAAAAAAAAAGGAAAAAGGAAATTAATCATCATACCACTTT 531
QY      2543 CTTTAAATAGATCAATTAGCCAGCGTGTGCTCATCTGTATCCACACCTTTG 2602
Db      530 CTATATAAATCTTTTCTAGACAGGCACTGTGCTCATCTGTATCCACACCTTTG 471
QY      2603 GTAGGCTGAGTGTGATGATCACCCTGAGTCAAGAGTTTCAGTCCAGCTGGCAATATG 2662
Db      470 GGAGGCTGAGTGTGATGATCACCCTGAGTCAAGAGTTTCAGTCCAGCTGGCAATATG 411
QY      2663 CTGAAAACCTGTCTCTAATAAATTAATAAATTTAGCCGCGCATGTGTGCGAGTCTTGT 2722
Db      410 GTGAAAACCTGTCTCTAATAAATTAATAAATTTAGCCGCGCATGTGTGCGAGTCTTGT 351
QY      2723 AATCCAGCTACTTGGAGGCTGAGGAGGAGAAATCACTTGAACCGAGGAGGAGAGTT 2782
Db      350 AATTCAAGCTACTGAGGAGGCTGAGGAGGAGAAATCACTTGAACCGAGGAGGAGAGTT 291
QY      2783 GCACTGAGCTGAGATTGTGCTGCACTGCACTGCACTGGGCAAGCAAACTCTGTC 2842
Db      290 TCAGTGAAGCTGAGACTGCACTGCACTTGTACTCCAGCTGGAACAAGAGCAAACTCTGTC 231
QY      2843 TGGAAAAAAAAAAAAAAAA 2859
Db      230 TCAAAAAAAAAAAAAAAA 214

RESULT 8
US-11-412-373-1/c
; Sequence 1, Application US/11412373
; Publication No. US20060189793A1
; GENERAL INFORMATION:
; APPLICANT: Yen, Frances
; APPLICANT: Denison, Blake
; APPLICANT: Bour, Barbara
; APPLICANT: Bihain, Bernard
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Edbeets-Reed, Dana
; APPLICANT: Salter-Cid, Luisa
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITTING NEOPLASTIC
; FILE REFERENCE: 89 US2 CIP
; CURRENT APPLICATION NUMBER: US/11/412,373
; CURRENT FILING DATE: 2006-04-27
; PRIOR APPLICATION NUMBER: US/10/121,034
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US/09/750,580
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 09/599,362
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: PCT/IB00/0101
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: PCT/IB99/02058
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 49/469/099
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 60/113,686
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 60/141,032
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 81001
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: 10946..112946
; OTHER INFORMATION: 5'regulatory region
; FEATURE:
;
; NAME/KEY: exon
; LOCATION: 12947..12958
; OTHER INFORMATION: exon 1
; FEATURE:
; NAME/KEY: exon
; LOCATION: 13470..13526
; OTHER INFORMATION: exon 2
; FEATURE:
; NAME/KEY: exon
; LOCATION: 13641..13752
; OTHER INFORMATION: exon 3
; FEATURE:
; NAME/KEY: exon
; LOCATION: 14271..15968
; OTHER INFORMATION: exon 4
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 15969..17969
; OTHER INFORMATION: 3'regulatory region
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1239
; OTHER INFORMATION: 20-828-311 : polymorphic base C or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 12347
; OTHER INFORMATION: 17-42-319 : polymorphic base C or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 15241
; OTHER INFORMATION: 17-41-250 : polymorphic base C or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 42218
; OTHER INFORMATION: 20-841-149 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 45442
; OTHER INFORMATION: 20-842-115 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 77058
; OTHER INFORMATION: 20-853-415 : polymorphic base C or T
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 929..949
; OTHER INFORMATION: 20-828.pu
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1357..1377
; OTHER INFORMATION: 20-828.rp complement
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 12029..12050
; OTHER INFORMATION: 17-42.pu
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 12581..12603
; OTHER INFORMATION: 17-42.rp complement
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 14992..15012
; OTHER INFORMATION: 17-41.pu
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 15460..15482
; OTHER INFORMATION: 17-41.rp complement
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 42070..42090
; OTHER INFORMATION: 20-841.pu
; FEATURE:
; NAME/KEY: primer_bind
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OTHER INFORMATION: 20-841.rp	
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NAME/KEY: primer_bind	
LOCATION: 45863..45883	complement
OTHER INFORMATION: 20-842.rp	
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NAME/KEY: primer_bind	
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NAME/KEY: primer_bind	
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NAME/KEY: primer_bind	
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NAME/KEY: primer_bind	
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NAME/KEY: primer_bind	
LOCATION: 15242..15260	
OTHER INFORMATION: 17-41-250.mis	complement
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NAME/KEY: primer_bind	
LOCATION: 42199..442317	
OTHER INFORMATION: 20-841-149.mis	
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NAME/KEY: primer_bind	
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OTHER INFORMATION: 20-841-149.mis	complement
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NAME/KEY: primer_bind	
LOCATION: 45423..45441	
OTHER INFORMATION: 20-842-115.mis	
FEATURE:	
NAME/KEY: primer_bind	
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OTHER INFORMATION: 20-853-415.mis	
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OTHER INFORMATION: 20-853-415.mis	complement
FEATURE:	
NAME/KEY: misc_binding	
LOCATION: 1227..1251	
OTHER INFORMATION: 20-828-311.probe	
FEATURE:	
NAME/KEY: misc_binding	
LOCATION: 12335..12359	

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? OTHER INFORMATION: 17-43-319.probe
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? FEATURE:
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? NAME/KEY: misc binding
? LOCATION: 15229..1523
? OTHER INFORMATION: 17-41-250.probe
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? NAME/KEY: misc binding
? LOCATION: 42206..42230
? OTHER INFORMATION: 20-841-149.probe
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Query Match	8.6%	Score 247;	DB 7;	Length 81001;
Best Local Similarity	86.6%	Pred. No. 2.1e-26;		
Matches 271; Conservative	1;	Mismatches 41;	Indels 0;	Gaps 0;

Qy	2547	AAATAGAAATCATTAAGCCAGGGGTGGTGCATCTTGTAATCCACACACTTTGGTGG	2606
Db	65051	ATAAGGAATTTGTGTGGCCAGGTGCAGTGGCTACGCCCTGTAAATCCAGACACTTTGGGAG	64992
Qy	2607	GCTGAGGTGTGGGATCACCTTGAGGTCAAGAGTTTCAGATCCAGCCTGGCCAAATATGTCTGA	2666
Db	64991	GCCAAGGTGTGTGGATCACCCTGAGGTCAAGAGTTTCAGACCAAGCCTGGCCAAATATGTGA	64933
Qy	2667	AACCTGTCTCTACTAAATTTACAAAATTAGCCGGCCATGTGTGGCAGGTGCTTGTAAATC	2726
Db	64931	AACCCGCTCTCTATTAAAAATACAAAATTAGCCGGGCATGTGTGGCAGGACCTGTAAATC	64872
Qy	2727	CCAGCTACTTGGGAGGTGAAGGACGAGAGAAATCACTTGAACCAAGAAAGGAGAGGTGGAC	2786
Db	64871	CCAGCTACTCAGGAGGCTGAAGGACGAGAGAAATCACTTGAACCCGGGAGGGCGAGGTTGGACG	64812
Qy	2787	TGAGCTGAGATTGGCCACTGCACCTCCAGCCTGGGCAACAAGAGCAAACTGTGTCTGGA	2846
Db	64811	TGAGCTGAGATTGGCCACTGCACCTCCAGCCTGGGCAACAAGAGCAAGACTGTATTCAA	64755
Qy	2847	AAAAAAAAAAAAA	2859
Db	64751	AAAAAAAAACAAA	64739

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1 RESULT 9 US-10-669-920-341/c
2 Sequence 341, Application US/10669920
3 Publication No. US20060194265A1
4 GENERAL INFORMATION:
5 APPLICANT: Morris, David W.
6 APPLICANT: Malandino, Marc S.
7 TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
8 FILE REFERENCE: 20366-066001
9 CURRENT APPLICATION NUMBER: US/10/669,920
10 CURRENT FILING DATE: 2003-09-23
11 PRIOR APPLICATION NUMBER: US 10/004,113
12 PRIOR FILING DATE: 2001-10-23
13 PRIOR APPLICATION NUMBER: US 10/052,482
14 PRIOR FILING DATE: 2001-11-08
15 PRIOR APPLICATION NUMBER: US 09/997,722
16 PRIOR FILING DATE: 2001-11-30
17 PRIOR APPLICATION NUMBER: US 10/034,650
18 PRIOR FILING DATE: 2001-12-20
19 PRIOR APPLICATION NUMBER: US 10/085,117
20 PRIOR FILING DATE: 2002-02-27
21 PRIOR APPLICATION NUMBER: US 10/087,192
22 PRIOR FILING DATE: 2002-03-01
23 PRIOR APPLICATION NUMBER: US 10/322,281
24 PRIOR FILING DATE: 2002-12-17
25 PRIOR APPLICATION NUMBER: US 10/322,696
26 PRIOR FILING DATE: 2002-12-17
27 NUMBER OF SEQ ID NOS: 1441
28 SOFTWARE: FastSeq for Windows Version 4.0
29 SEQ ID NO 341
30 LENGTH: 438732
31 TYPE: DNA
32 ORGANISM: Homo sapiens

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QY 2743 CTGAGGACGAGAGATCACTTGAACCAAGAAAGGAGGTTGCACTGAGCTGAGATTGTGC 2802  
DB 614 CTGAGGACGAGAGATCACTTGAACCAAGAAAGGAGGTTGCACTGAGCTGAGATTGTGC 555  
QY 2803 CACTGCACTCCAGCTGGGCGAACAAGCAAACTCTGTCTGGAAAAA 2859  
DB 554 CACTGCACTCCAGCTGGGCGAACAAGCAAACTCTGTCTCAAAAAA 498

## RESULT 12

US-11-266-748A-404879  
; Sequence 404879, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; PRIOR FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 48396  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 404879  
; LENGTH: 1000  
; TYPE: DNA  
; ORGANISM: Homo Sapiens

US-11-266-748A-404879

Query Match 8.6%; Score 245.4; DB 8; Length 1000;

Best Local Similarity 88.9%; Pred. No. 8.8e-26; Matches 264; Conservative 1; Mismatches 32; Indels 0; Gaps 0;

QY 2563 GCCAGGCGTGTGCTCATCTTGTATCCAGACACTTGTAGGCTGAGGTGGTGGAT 2622  
DB 207 GCCAGGCGTGTGCTCATCTTGTATCCAGACACTTGTAGGCTGAGGTGGTGGAT 266  
QY 2623 CACTGAGGTGAGAGTTGAGTCCAGCTGGCCCAATATCTGAAACCTGTCTTACTA 2682  
DB 267 CACTGAGGTGAGAGTTGAGTCCAGCTGGCCCAATATGATGAAACCTGTCTTACTA 326  
QY 2683 AAATTCAAAAATTAGCCCGCCATGTGTGAGGCTTGTAAATCCAGCTCACTTGGGAAG 2742  
DB 327 AAATTCAAAAATTAGCCCGCCATGTGTGAGGCTTGTAAATCCAGCTCACTTGGGAAG 386  
QY 2743 CTGAGGACGAGAGATCACTTGAACCAAGAAAGGAGGTTGCACTGAGCTGAGATTGTGC 2802  
DB 387 CTGAGGACGAGAGATCACTTGAACCAAGAAAGGAGGTTGCACTGAGCTGAGATTGTGC 446  
QY 2803 CACTGCACTCCAGCTGGGCGAACAAGCAAACTCTGTCTGAAAAA 2859  
DB 447 CACTGCACTCCAGCTGGGCGAACAAGCAAACTCTGTCTCAAAAAA 503

## RESULT 13

US-11-266-748A-475925/c

; Sequence 475925, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; PRIOR FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 48396  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 475925  
; LENGTH: 1000  
; TYPE: DNA  
; ORGANISM: Homo Sapiens

US-11-266-748A-475925

Query Match 8.6%; Score 245.4; DB 8; Length 1000;

Best Local Similarity 88.9%; Pred. No. 8.8e-26; Matches 264; Conservative 1; Mismatches 32; Indels 0; Gaps 0;

QY 2563 GCCAGGCGTGTGCTCATCTTGTATCCAGACACTTGTAGGCTGAGGTGGTGGAT 2622  
DB 794 GCCAGGCGTGTGCTCATCTTGTATCCAGACACTTGTAGGCTGAGGTGGTGGAT 735  
QY 2623 CACTGAGGTGAGAGTTGAGTCCAGCTGGCCCAATATCTGAAACCTGTCTTACTA 2682  
DB 734 CACTGAGGTGAGAGTTGAGTCCAGCTGGCCCAATATGATGAAACCTGTCTTACTA 675  
QY 2683 AAATTCAAAAATTAGCCCGCCATGTGTGAGGCTTGTAAATCCAGCTCACTTGGGAAG 2742  
DB 674 AAATTCAAAAATTAGCCCGCCATGTGTGAGGCTTGTAAATCCAGCTCACTTGGGAAG 615  
QY 2743 CTGAGGACGAGAGATCACTTGAACCAAGAAAGGAGGTTGCACTGAGCTGAGATTGTGC 2802  
DB 614 CTGAGGACGAGAGATCACTTGAACCAAGAAAGGAGGTTGCACTGAGCTGAGATTGTGC 555  
QY 2803 CACTGCACTCCAGCTGGGCGAACAAGCAAACTCTGTCTGAAAAA 2859  
DB 554 CACTGCACTCCAGCTGGGCGAACAAGCAAACTCTGTCTCAAAAAA 498

## RESULT 14

US-10-540-898-374

; Sequence 374, Application US/10540898  
; Publication No. US20060166213A1  
; GENERAL INFORMATION:  
; APPLICANT: David W. Morris  
; APPLICANT: Marc Malandro  
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer  
; FILE REFERENCE: CHIR0056-101 (P023367.0003)  
; CURRENT APPLICATION NUMBER: US/10/540,898  
; PRIOR FILING DATE: 2005-06-27  
; PRIOR APPLICATION NUMBER: US 10/330,773  
; PRIOR FILING DATE: 2002-12-27

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; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 374
; LENGTH: 225587
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) ... (225587)
; OTHER INFORMATION: n = A,T,C or G
US-10-540-898-374

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Query Match      8.6%; Score 244.8; DB 6; Length 225587;
Best Local Similarity 84.8%; Pred. No. 3.5e-26;
Matches 273; Conservative 1; Mismatches 48; Indels 0; Gaps 0;

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QY 2537 ATTTCTTTAAATAGATCATTAGGCGCGGTGCTCATGCTTTGTAATCCAGC 2596
DB 139637 ATTTTAAATATAATTTTAAATTTGGCGCGGTGCTCATGCTTTGTAATCCAGC 139636
QY 2597 ACTTTGAGGCTGAGGTGCTGATCAGCTGAGGTGAGGATTTCCAGTCCAGCTGGCC 2656
DB 139697 ACTTTGAGGCTGAGGTGCTGATCAGCTGAGGTGAGGATTTCCAGTCCAGCTGGCC 139756
QY 2657 AATATGCTGAACCCCTGCTCTCTAATAAATTACAAAATTAGCCGATGCTGGCAGGT 2716
DB 139757 AATATGCTGAACCCCTGCTCTCTAATAAATTAGCCGATGCTGGCAGGT 139816
QY 2717 GCTTGTATCCAGCTACTTGGAGGCTGAGGAGGATCACTTGAACGAGAGGCA 2776
DB 139817 GCTTGTATCCAGCTACTTGGAGGCTGAGGAGGATCACTTGAACGAGAGGCA 139876
QY 2777 GAGTTGCACTGAGCTGAGTGTGCACTGCACTCCAGCTGGGCAACAGAGCAAAAC 2836
DB 139877 GAGTTGCACTGAGCTGAGTGTGCACTGCACTCCAGCTGGGCAACAGAGCAAAAC 139936
QY 2837 TCTGCTGAGAAAAAATAA 2858
DB 139937 TCTGCTGAGAAAAAATAA 139958

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RESULT 15
US-10-669-920-1403/c
; Sequence 1403, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Moritz, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669, 920
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1403
; LENGTH: 84105
; TYPE: DNA

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; ORGANISM: Homo sapiens
US-10-669-920-1403

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Query Match      8.6%; Score 244.4; DB 6; Length 84105;
Best Local Similarity 85.0%; Pred. No. 4.8e-26;
Matches 272; Conservative 1; Mismatches 47; Indels 0; Gaps 0;

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QY 2539 TTTCTTTAAATAGATCATTAGGCGCGGTGCTCATGCTTTGTAATCCAGC 2598
DB 69319 TTTACTTTAAATAAATAAATAAATAGGCTGGCGGTGCTCATGCTTTGTAATCCAGC 69260
QY 2599 TTTGTAAGCTGAGGTGCTGATCAGCTGAGGTGAGGATTTCCAGTCCAGCTGGCC 2658
DB 69259 ATTGGAGGCGCGGCGGCGGATCACTGAGGTGAGGATTTCCAGTCCAGCTGGCC 69200
QY 2659 TATGCTGAACCCCTGCTCTAATAAATTAGCCGCGCATGCTGGCAGGTCG 2718
DB 69199 CGTGTGAACCCCTGCTCTAATAAATTAGCCGCGCATGCTGGCAGGTCG 69140
QY 2719 TTGTAATCCAGCTACTTGGAGGCTGAGGAGGATCACTTGAACGAGAGGCA 2778
DB 69139 CTGTAATCCAGTACTTGGAGGCTGAGGAGGATTTGTAACAGGAGGCA 69080
QY 2779 GGTGCACTGAGCTGAGTGTGCACTGCACTCCAGCTGGGCAACAGAGCAAACTC 2838
DB 69079 GGTGCACTGAGCTGAGTGTGCACTGCACTCCAGCTGGGCAACAGAGTGAATC 69020
QY 2839 TCTGCTGAGAAAAAATAA 2858
DB 69019 TCTGCTGAGAAAAAATAA 69000

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Search completed: October 14, 2006, 14:44:00  
Job time : 573 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus.p2n model

Run on: October 14, 2006, 14:05:08 ; Search time 1043 Seconds  
(without alignments)  
6307.111 Million cell updates/sec

Title: US-10-667-289-2  
Perfect score: 3326  
Sequence: 1 MNXVTIQMDAVIALYILFSW.....TYFPQNILSHFNRLSLK 629

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues  
Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODE=frame+.p2n.model -DRV=xlh  
-Q=/abses/ABSSMBR.epool/US10667289/runcat\_13102006\_111531\_24352/app\_query.fasta\_1  
-DB=N Geneseq -OPT=fastcap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blonsum62 -TRANS=human40.cdi -LIST=45  
-DOCLIGN=200 -THR SCORE=pcr -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTPRT=prc -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abses02h  
-USER=US10667289\_@CGN\_1\_1\_161\_@runcat\_13102006\_111531\_24352 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Geneseq\_8:\*  
1: geneseqn1980s:\*  
2: geneseqn1980s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*  
15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3324	99.9	2859	6	AAK98257 Human DNA
2	3324	99.9	2859	13	AD573604 Human IL-
3	3324	99.9	2859	14	AA51089 Human DNA

4	3314	99.6	1890	14	ADV43392 Human pay
5	3314	99.6	1910	5	AAFB822 Human hae
6	3314	99.6	2830	5	AAFB8773 Human hae
7	3292	99.0	2123	5	AAFB87820 Human hae
8	2952	88.8	1698	6	AAFB8774 Human hae
9	2747	82.6	1887	6	AAK98258 Human DNA
10	2280.5	68.6	1935	6	AAFB8777 Mouse hae
11	2192	65.9	1301	5	AAFB87821 Human hae
12	2175	65.4	1479	5	AAFB87819 Human hae
13	2039	61.3	1155	4	AAFB88149 Human hae
14	2039	61.3	1155	10	ADFC07176 DNA encod
15	2039	61.3	1155	14	AD265011 DNA cyto
16	1868	56.2	1071	6	AAFB8775 Human hae
17	1747	52.5	1152	4	AAFB88150 Human DNA
18	1747	52.5	1152	4	ADFC07178 Human DNA
19	1747	52.5	1152	14	AD265013 Reverse t
20	1695	51.0	1784	5	AAFB87818 Human hae
21	286	8.6	360	5	AAFB87833 Human hae
22	256.5	7.7	2995	2	AAQ27656 gp130. 2/
23	256.5	7.7	2995	3	AA240299 Mouse gp1
24	256.5	7.7	2995	13	AD66595 Murine in
25	250	7.5	412	4	ABA46474 Human bre
26	225.5	6.8	3053	10	AD552498 Primary r
27	225.5	6.8	3053	13	AD66593 Rat inter
28	221	6.6	4023	6	ABQ78355 Nucleotid
29	216	6.5	2589	14	ADV43358 Human pay
30	216	6.5	3400	12	ADK90589 Human IL-
31	216	6.5	3400	12	ADM33786 Human IL-
32	216	6.5	4040	2	AA159731 Human int
33	216	6.5	4040	3	AA35207 Human ade
34	216	6.5	4040	3	AA21329 Human low
35	216	6.5	4040	6	ABK84394 Human CDN
36	216	6.5	4040	10	AD39703 Human int
37	216	6.5	4040	10	ADFB76394 Novel hum
38	216	6.5	4040	10	AB297023 Human nuc
39	216	6.5	4040	11	ABD20872 Human pul
40	216	6.5	4040	12	AD019579 Human PRO
41	216	6.5	4040	13	ADP54648 Human PRO
42	216	6.5	4040	14	ADY15767 DNA encod
43	216	6.5	4040	14	ADY19579 DNA encod
44	216	6.5	4040	14	ADY86629 Human int
45	216	6.5	4040	15	AE884947 IMPDH mar

## ALIGNMENTS

RESULT 1	ID	AAK98257 standard; cDNA; 2859 BP.	ADV43392 Human pay
AAK98257	AAK98257	28-MAY-2002 (first entry)	AAFB822 Human hae
XX	XX		AAFB8773 Human hae
AC	XX		AAFB87820 Human hae
XX	XX		AAFB8774 Human hae
DT	XX		AAK98258 Human DNA
XX	XX		AAFB8777 Mouse hae
DE	XX		AAFB87821 Human hae
XX	XX		AAFB87819 Human hae
XX	XX		AAFB88149 Human hae
OS	XX		ADFC07176 DNA encod
XX	XX		AD265011 DNA cyto
FH	XX		AAFB8775 Human hae
FT	XX		AAFB88150 Human DNA
FT	XX		ADFC07178 Human DNA
FT	XX		AD265013 Reverse t
FT	XX		AAFB87818 Human hae
FT	XX		AAFB87833 Human hae
FT	XX		AAQ27656 gp130. 2/
FT	XX		AA240299 Mouse gp1
FT	XX		AD66595 Murine in
FT	XX		ABA46474 Human bre
FT	XX		AD552498 Primary r
FT	XX		AD66593 Rat inter
FT	XX		ABQ78355 Nucleotid
FT	XX		ADV43358 Human pay
FT	XX		ADK90589 Human IL-
FT	XX		ADM33786 Human IL-
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FT	XX		AA35207 Human ade
FT	XX		AA21329 Human low
FT	XX		ABK84394 Human CDN
FT	XX		AD39703 Human int
FT	XX		ADFB76394 Novel hum
FT	XX		AB297023 Human nuc
FT	XX		ABD20872 Human pul
FT	XX		AD019579 Human PRO
FT	XX		ADP54648 Human PRO
FT	XX		ADY15767 DNA encod
FT	XX		ADY19579 DNA encod
FT	XX		ADY86629 Human int
FT	XX		AE884947 IMPDH mar

FT                   sig\_peptide                   /note= "Xaa= Arg or Gly"  
 FT                   119. .187  
 FT                   /\*tag= b  
 FT                   127  
 FT                   misc\_feature                   /\*tag= c  
 FT                   /Note= "If the base at this position is G (encoding Gln),  
 FT                   the base at position 563 is also G (encoding Gly). If the  
 FT                   base at this position is T (encoding His) the base at  
 FT                   position 563 is A (encoding Arg)"  
 FT                   188. .2005  
 FT                   /\*tag= d  
 FT                   /Note= "Mature DCRS5 protein"  
 FT                   563  
 FT                   misc\_feature                   /\*tag= e  
 FT                   /Note= "If the base at this position is G (encoding Gly),  
 FT                   the base at position 127 is also G (encoding Gln). If the  
 FT                   base at this position is A (encoding Arg) the base at  
 FT                   position 127 is T (encoding His)"

PN                   MO200185790-A2.

XX                   15-NOV-2001.

XX                   10-MAY-2001; 2001MO-US015057.

XX                   10-MAY-2000; 2000US-0203426P.

XX                   (SCHE ) SCHERING CORP.

XX                   Chirica M, Kaetelein RA, Moore KM, Parham CL;

XX                   WPI; 2002-062238/08.

XX                   P-PSDB; AA014008.

PT                   Novel DNA cytokine receptor subunit 5 polypeptide which is subunit of  
 receptor complex for p40/IL-830, useful for treating conditions  
 associated with abnormal expression or triggering of response to p40/IL-  
 B30 ligand.

XX                   Claim 18; Page 9-12; 74pp; English.

XX                   The present cDNA sequence encodes the human DNA cytokine receptor  
 subunit 5 (defined as DCRS5 or IL30 receptor) of the invention. DCRS5 is  
 a member of the class I branch of the cytokine receptor superfamily and  
 is closely related to the IL-6 receptor subunit gp130 and the IL-12R-Beta  
 -2 subunit. Cytokines are soluble molecules which play a critical role in  
 controlling the complex cellular interactions of the immune response. The  
 invention comprises novel receptors related to cytokine receptors  
 designated DNA cytokine receptor subunits (DCRS). Specifically the  
 invention comprises a subunit (DCRS5) for a receptor complex for the  
 p40/IL-B30 ligand. The DCRS5 proteins of the invention are useful for  
 treating diseases or disorders associated with abnormal expression or  
 abnormal triggering of response to the p40/IL-B30 ligand. The proteins of  
 the invention can be used to modulate the physiology or development of a  
 cell from a host which exhibits Th1-mediated disease; multiple sclerosis;  
 rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 diabetes; psoriasis; sepsis; an allogeneic transplant recipient; chronic  
 Th2 response; tumor; viral or fungal growth; vaccine recipient; or an  
 allergic response

XX                   Sequence 2859 BP; 929 A; 575 C; 560 G; 791 T; 0 U; 4 Other;

XX                   SQ

Alignment Scores:  
 Prod. No.:                   4,9e-304                   Length:                   2859  
 Score:                   3324.00                   Matches:                   629  
 Percent Similarity:                   100.0%                   Conservative:                   0  
 Best Local Similarity:                   100.0%                   Mismatch:                   0  
 Query Match:                   99.9%                   Indels:                   0  
 DB:                   6                   Gaps:                   0

US-10-667-289-2 (1-629) x AAK98257 (1-2859)

QY                   1 MetAsn\*\*ValThrIleGlnTrpAspAlaValIleAlaLeuTyrIleLeuPheSerTrp 20

DB                   119 ATGAATCAAGTCATATTCATGAGGATGAGCAAGTAATGACCCCTTACATCTTCACCTGG 178  
 QY                   21 CYNHIEGLVGIYIIEThraenIleAenCysSerGlyVHIEIIETrpValGluProAlaThr 40  
 DB                   179 TGTCAATGAGGAAATTCATTAATTAATCTCTGCGCACATCTGGGTATACACAGCACAC 238  
 QY                   41 IIEPheLysMetGlyMetAsnIleSerIIETrpCysGlnAlaAlaIIElyAsnCysGln 60  
 DB                   239 ATTTTAATATGAGTATGATATATCTATATATATTCCTCAAGACGACATTTAAGAACTGCCAA 298  
 QY                   61 ProAlaLysLeuHisPheTyrLysAsnGlyIIElyGluAlaGluPheGlnIIEThraGlie 80  
 DB                   299 CCAAGGAACCTTCATTTTATATAAAATGACATCAAGAAAGATTTCAATTCACAGAGATT 358  
 QY                   81 AsnLysThrAlaArgLeuTrpTyrLysAsnPheLeuGluProHisAlaSerMetTyr 100  
 DB                   359 AATTAACACACAGCTGGCTTGGTATTAACATTTCTGGAACACATCTCTATATGTC 418  
 QY                   101 CysThrAlaGluCysProLysHisPheGlnGluThrLeuIIECysGlyLysAspIIESer 120  
 DB                   419 TGCATGCTGAAATGTCCCAACATTTTCAAGAGACACTGATATGTGAAAGACATTTCT 478  
 QY                   121 SerGlyTyrProProAspIIEProAspGluValIIEThraValIIETrpGluTyrSerGly 140  
 DB                   479 TCGATATTCGCGCAATATCTCTGATGAAAGTAACTGTGCTATTTATATAATTTACAGC 538  
 QY                   141 AsnMetThrCysThrTrpAsnAla\*\*LysLeuThrTyrIIEAspThrLysTyrValIIE 160  
 DB                   539 AACATACCTTGACCTCGAATGCTRGAAGCTCACTACATAGACACAAATAACGTGATA 598  
 QY                   161 HisValLysSerLeuGluThrGluGluGlnGlnIIETrpLeuThrSerSerTyrIIEAsn 180  
 DB                   599 CATGTAAAGATTTAAGACAGAAAGAGACAAAGATATCTCACTCAAGCATATATTAAC 658  
 QY                   181 IIESerThrAspSerLeuGlnGlyLysLysTyrLeuValIIETrpAlaGlnAlaAsn 200  
 DB                   659 ATCTCCACGATTCATTAAGGTGCAAGAGTACTCTGTGGGTCCCAAGCAGCAAAC 718  
 QY                   201 ALIEuGlyMetGluSerLysGlnLeuGlnIIEHisLeuAspAspIIEValIIEPro 220  
 DB                   719 GCACCTGAGCATGAGAAAGTCAAACAACTGCAATTCACCTGATATATAGTATACCT 778  
 QY                   221 SerAlaAlaValIIESerAlaGluThrIIEAsnAlaThrValProLysThrIIEIIE 240  
 DB                   779 TCTGACGCGGTATTTCCAGGCTGAGCATTAATAGCTACAGTCCCAAGACCAATAAT 838  
 QY                   241 TyrTrpAspSerGlnThrThrIIEGlyLysValIIESerCysGluMetArgTyrLysAlaThr 260  
 DB                   839 TATTTGGATATGTCAAACAAATTTGAAAGGTTCTGTGAAATGAGATCAAGGCTTAC 898  
 QY                   261 ThrAsnGlnThrTrpAsnValIIEGluPheAspThrAsnPheThrTyrValIIEGlnIIE 280  
 DB                   899 ACAACCAAACTTGAAATGTTAAAGATTTGACACCAATTTTACATATGTGCAACAGTCA 958  
 QY                   281 GluPheTyrLeuGluProAsnIIElyTyrValIIEGlnValArgCysGlnGluThrGly 300  
 DB                   959 GAATTCATCTGAGGCAACATTAAGTACGTATTTCAAGTGAAGATGCAAGAAAGAGC 1018  
 QY                   301 LysAlaTyrTrpGlnProTrpSerSerProPhePheHisLysThrProGluThrValPro 320  
 DB                   1019 AAAAGTACTGAGGAGCTTGAGGTTCCCGTTTTCATATAAACACCTGAAACAGTTCCC 1078  
 QY                   321 GlnValThrSerLysAlaPheGlnHisAspThrTrpAsnSerGlyLeuThrValAlaSer 340  
 DB                   1079 CAGGTACATCAAAAGCATTTCCACATGACATGAGAAATTCGGGTACACAGTTGCTTCC 1138  
 QY                   341 IIESerThrGlyHisLeuThrSerAspAsnArgGlyAspIIEGlyLeuLeuLeuGlyMet 360  
 DB                   1139 ATCTTACAGGAGCACTTACTCTGACAAACAGAGAGACATTTGAGCTTTATTTGGGAATG 1198  
 QY                   361 IIEValPheAlaValMetLeuSerIIELeuSerLeuIIEGlyIIEPheAsnArgSerPhe 380

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Qy      381 ArgThrGlyIleYsaGArgIleLeuLeuLeuIleProIysrPleuYrGluAspIle 400
Db      1259 CGAACTGGGATTAAAGAGGATCTTATTTGTTAATACCAAGTGGCTTTATGAAAGATATT 1318
Qy      401 ProAsnMetIysAsnSerAsnValValIlyMetLeuGlnGluAsnSerGluLeuMetAsn 420
Db      1319 CTTAATATGAAAAACAGCAATGTTGTGAAATGTCTACAGGAAATATGAACTTATCAAT 1378
Qy      421 AsnAsnSerSerGluGlnValIleuYrValAspProMetIleThrGluIleYrGluIle 440
Db      1379 AATAATTTCCAGTGAGGAGTCTTATATGTTGATCCCATGTGATTCAGAGATAAAGAAATC 1438
Qy      441 PheIleProGluIleYsIlyrProThrAspYrIlyrGluGlnGluAsnThrGluThr 460
Db      1439 TTCAATCCCAAGAACCAAGCCTACAGACTACAGAGAGAAATACAGAGACCCCTGGAGACA 1498
Qy      461 ArgAspYrProGlnIleAsnSerIleuPheAspAsnThrValValIlyrIleProAspLeu 480
Db      1499 AGAGACTACCCGCAAACTGCTATTGACAAATACATCACTGTTGATATATTCGATCTC 1558
Qy      481 AsnThrGlyIlyrIlyrProGlnIleSerAsnPheLeuProGluGlySerHisIleuSerAsn 500
Db      1559 AACACTGATATTAACCCCAATTTTCAATTTCTGCTGAGGAGAACCCATCTCAGCAAT 1618
Qy      501 AsnAsnGluIleThrSerIleuThrIleuYrProIleAspSerIleuAspSerGlyAsn 520
Db      1619 AATAATGAATATTTCTCTTAACCTTAACCAACCACTTAATTTCTTAAGCTCAGGAAAT 1678
Qy      521 AsnProArgLeuGlnIlyrHisProAsnPheAlaPheSerValSerSerValAsnSerLeu 540
Db      1679 AATCCCAAGTTACAAAGCATCTTAATTTGCTTTTCTGTTCAAGTGAATTCATCTA 1738
Qy      541 SerAsnThrIlePheLeuGlyIleuSerIleuIleuAsnGlnGlyIleuYrGlySerSer 560
Db      1739 AGCAACCAATATTTCTTGAGAAATTAAGCCTCATATTAATCAAGAGAAATCAGATTCCT 1798
Qy      561 ProAspIleGlnAsnSerValIleuGluGlnThrThrMetLeuLeuGluAsnAspSerPro 580
Db      1799 CCGACATACAAACCTCAGTAGAGGAGGAAACCAACATGCTTTGGAAAAATGATTCACCC 1858
Qy      581 SerGluThrIleProGluGlnThrIleuProAspGluPheValSerCysLeuGlyIle 600
Db      1859 AGTGAACCTATTCCAGAACAGACCTCTCTCTGATTAATTTGCTCTCTGTTGGGATC 1918
Qy      601 ValAsnGluIleuProSerIleAsnThrYrPheProGlnAsnIleuGluSerHis 620
Db      1919 GTGAATGAGAGATTGGCATCTAATTAATCTTATTTCCACAAAATATTTTGGAAAGCCAC 1978
Qy      621 PheAsnArgIleSerLeuLeuGluIlyr 629
Db      1979 TTCAATAGATTTCACTCTTGAAAAAG 2005

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RESULT 2  
ADST73604  
ID ADST73604 standard; cDNA; 2859 BP.

ADST73604;  
16-DEC-2004 (first entry)

Human IL-23R coding sequence.  
ss; gene; human; interleukin 23; subunit p19; IL-23; IL-23p19; tumour;  
growth; agonist; antagonist; receptor; cancer; antigen-binding site;  
antibody; extracellular region; antisense nucleic acid;  
small interference RNA; siRNA; polyclonal; monoclonal; humanized; Fab;  
Fv; F(ab')<sub>2</sub>; peptide mimetic; colon; ovarian; breast; melanoma; cachexia;  
anorexia; angiogenesis; gastrointestinal tract; respiratory tract;  
reproductive system; endocrine system.

Homo sapiens.

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XX      Key      Location/Qualifiers
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FT      /product= "IL-23R"
FT      sig_peptide 119..187
FT      /tag= a
FT      mat_peptide 188..2005
FT      /tag= c
XX      PN      MO2004081190-A2.
XX      PD      23-SEP-2004.
XX      PF      09-MAR-2004; 2004MO-US007198.
XX      PR      10-MAR-2003; 2003US-0453672P.
XX      PA      (SCHE ) SCHERING CORP.
XX      PI      Ofc M, Mcclanahan TK;
XX      DR      WPI; 2004-668951/55.
XX      DR      P-PSDB; ADST73605.
XX      PT      Modulating tumor growth, useful for treating a subject suffering from
PT      cancer or tumor, comprises contacting a tumor cell with an agonist or
PT      antagonist of IL-23.
XX      PS      Claim 4; SEQ ID NO 5; 57pp; English.
XX      CC      This sequence encodes human interleukin 23 receptor (IL-23R). The method
CC      of the invention for modulating tumour growth comprises contacting a
CC      tumour cell with an agonist or antagonist of IL-23. The agonist or
CC      antagonist is a binding composition which specifically binds the IL-23
CC      p19 subunit (IL-23p19) or the IL-23R protein. The identified agonist or
CC      antagonist may be used for diagnosing or treating a subject suffering
CC      from a cancer or tumour. The binding composition comprises an antigen-
CC      binding site of the antibody, an extracellular region of IL-23R, a small
CC      molecule, an antisense nucleic acid or small interference RNA (siRNA), or
CC      a detectable label. The binding composition comprises a polyclonal
CC      antibody, a monoclonal antibody, a humanized antibody or its fragment, a
CC      Fab, Fv, F(ab')2 fragment, or a peptide mimetic of an antibody. The
CC      tumour cell is a colon, ovarian or breast cancer cell, or melanoma cell.
CC      In the treatment method, the antagonist of IL-23 inhibits growth of
CC      cancer or tumour, cachexia, anorexia or angiogenesis. The cancer or
CC      tumour is of the gastrointestinal tract, respiratory tract, reproductive
CC      system or endocrine system. In diagnosing cancer or tumour, the binding
CC      composition comprises a nucleic acid probe or primer that specifically
CC      binds or hybridises to human or mouse IL-23p19 cDNA sequences, or the
CC      human IL-23R sequence.
XX      SQ      Sequence 2859 BP; 929 A; 575 C; 560 G; 791 T; 0 U; 4 Other;
XX
XX      Alignment Scores:
XX      Pred. No.: 4..9e-304 Length: 2859
XX      Score: 3324.00 Matches: 629
XX      Percent Similarity: 100.0% Conservative: 0
XX      Best Local Similarity: 100.0% Mismatches: 0
XX      Query Match: 99.9% Indels: 0
XX      DB: 13 Gaps: 0
XX
XX      US-10-667-289-2 (1-629) x ADST73604 (1-2859)
Qy      1 MetAsn**ValThrIleGlnTrpAspAlaValIleAlaLeuYrIleLeuPheSerTrp 20
Db      119 ATGAATCAAGTCACTATTCAATGGAGTGCAGTAAATGCCCTTACATTAATCTTCACTGG 178
Qy      21 CysHisGlyGlyIleThrAsnIleAsnCysSerGlyHisIleTrpValGluProAlaThr 40
Db      179 TGTCAATGAGAGGAAATTAACAATATTAACCTCTGCGCAATCTGGGTAAACCAAGCCACA 238
Qy      41 IlePheMetCylMetAsnIleSerIleYrCysGlnAlaIleAlaIleYsaEncyGln 60

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Db      239 ATTTTAAGATGGATGGAATATCTCATATATATGCGAACACAGCAATTAAAGAACTGCCAA 298
Qy      61  ProAluLeuHisPheTyrLysAsnGlyIleLeuGluLysPheGlnIleThrArgIle 80
Db      299 CCAAGGAACTTCATTTTATATAAATGCAATCAAGAAAGATTTCAATACACAGGATT 358
Qy      81  AsnLysThrThrAlaArgLeuTyrTyrLysAsnPheLeuGluProHisIleAsnMetTyr 100
Db      359 AATTAACAACACAGCTGGCTTTGGTATATAAAACCTTCTGGAACCACTGCTTATAGTAC 418
Qy      101 CysThrAlaGluCysProLysHisPheGlnGluThrLeuIleCysGlyLysAspIleSer 120
Db      419 TGCACGCTCAATGTCCTCAAAACATTTCAAGAGCACATGATATGTGAAAAAGCATTTCT 478
Qy      121 SerGlyTyrProProAspIleProAspGluValThrCysValIleTyrGluTyrSerGly 140
Db      479 TCTGGATATCCGGCCAGATATTTCTGATGAAGTAACCTGTGCATTTATGAATATTCAGGC 538
Qy      141 AsnMetThrCysThrTyrPheAsnAla**LysLeuThrTyrIleAspThrLysTyrValVal 160
Db      539 AACATGACTTGACCTCGAATTCGCGAAGCTCACCTACATAGCACAAAATACGTGTA 598
Qy      161 HisValLysSerLeuGluThrGluGluGluGlnGlnTyrLeuThrSerSerTyrIleAsn 180
Db      599 CATGTGAAGAGTTTGAAGACAGAAAGAACCAACAGATATCTCACCTCAACCTATATTAC 658
Qy      181 IleSerThrAspSerLeuGlnGlyLysLysLysTyrLeuValTyrValGlnAlaIleAsn 200
Db      659 ATCTCCACTATTCATTAACAAGGTGGCAAGATGCTTGTTGGTTCACAGCAAGCAAAAC 718
Qy      201 AlaLeuGlyMetGluSerLysGlnLeuGlnIleHisIleAsnAspAspIleValIlePro 220
Db      719 GCATGACGATGGAAGAGTCAAAACCACTCAATTCACCTGATGATATAGTATGATACCT 778
Qy      221 SerAlaAlaValIleSerArgIleGluThrIleAsnAlaThrValProLysThrIleIle 240
Db      779 TCTGCACCCGTCATTTCCAGGGCTGACATTAATCTACAGGCCCAAGACCATATATT 838
Qy      241 TyrThrAspSerGlnThrThrIleGluLysValSerCysGluMetArgTyrLysAlaThr 260
Db      839 TATTGGATAGTCAACAACAATTAAGAAAGGTTTCCGTGAATAAGATACAAAGGCTTACA 898
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Qy      281 GluPheTyrLeuGluProAsnIleLysTyrValPheGlnValArgCysGlnGluThrGly 300
Db      959 GAATTTCTACTTGAGCAACCAATTAAGTACGTATTTCAAGTGAAGATGTCAAGAAACAGGC 1018
Qy      301 LysArgTyrTyrGlnProTyrPheSerSerProPhePheHisLysThrProGluThrValPro 320
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Qy      321 GlnValThrSerLysAlaPheGlnHisAspThrTyrPheSerSerGlyLeuThrValAlaSer 340
Db      1079 CAGGTCACTCAATAAAGATTCACACAGACAGCAAGGATTTGGGCTTACAGTTGCTTCC 1138
Qy      341 IleSerThrGlyHisLeuThrSerAspAsnArgIleAspIleGlyLeuLeuLeuGlyMet 360
Db      1139 ATCTCTACAGGGCACCTTACTTCTGACACAGAGACACATGTGACCTTTATTGGGAATG 1198
Qy      361 IleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380
Db      1199 ATCGCTTTTGCTGTATGTTGTCATATCTTTCATTTGATGGAAATATTAACAGATCATTC 1258
Qy      381 ArgThrGlyIleLysArgArgIleLeuLeuLeuIleProLysTyrPleuTyrGluAspIle 400
Db      1259 CGAACTGGGATTAAAGAAGATCTTATGTTAATACCAAGTGGCTTTATGAAGATATT 1318
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Db      1379 AATTAATTCAGAGGAGAGGATCCCTATATGTTGATCCCATGATTAACAAGATTAAGAAATTC 1438
Qy      441 PheIleProGluHisLysProThrAspTyrTyrLysGluAsnThrGlyProLeuGluThr 460
Db      1439 TTCATCCCAAGAACACAAAGCTCACAGCTACAGAAAGAGAAATACAGAACCCCTCGAGACA 1498
Qy      461 ArgAspTyrProGluAsnSerLeuPheAspAsnThrThrValValTyrIleProAspLeu 480
Db      1499 AGAGACTTACCCGAAACCTCGCTATTGCAACATCTACAGTTGTATATTTCTGATCTTC 1558
Qy      481 AsnThrGlyTyrLysProGluIleSerAsnPheLeuProGluGlySerHisIleSerAsn 500
Db      1559 AACACGTGATATAAACCCCAATTTCAAAATTTTCTGCTGAGGGAAGCCATCTCAGCAAT 1618
Qy      501 AsnAsnGluIleThrSerLeuThrLeuLysProProValAspSerLeuAspSerGlyAsn 520
Db      1619 AATTAATGAATTAATCTTCTTAACATTAACCAACAGTGAATCTTGAACCTCAGAGAAAT 1678
Qy      521 AsnProArgLeuGlnLysHisProAsnPheAlaPheSerValSerSerValAsnSerLeu 540
Db      1679 AATCCAGGTACAAAGACATCTTAATTTTGCTTTTCTGTTTCAAGTGTGAATTCACATA 1738
Qy      541 SerAsnThrIlePheLeuGlyGluLeuSerLeuIleLeuAsnGlnGlyLysCysSerSer 560
Db      1739 AGCAACACATATTTCTTGAGAAATTAACCTTCATTAATCAAGAGAAATGCAAGTTCT 1798
Qy      561 ProAspIleGlnAsnSerValGluGluGluThrThrMetLeuLeuGluAsnAspSerPro 580
Db      1799 CCGACATACAAACCTCAGTAGAGAGAAACCAACATCTTTGGAAAAATGATTCACCC 1858
Qy      581 SerGluThrIleProGluGlnThrLeuLeuProAspGluPheValSerCysLeuGlyIle 600
Db      1859 AGTGAACATATTCACAAACAGACCTCTTCTCGATGAATTTGTCCTGCTTTGGGGAATC 1918
Qy      601 ValAsnGluGluLeuProSerIleAsnThrTyrPheProGluAsnIleLeuGluSerHis 620
Db      1919 GTGAATGAGAGTTGCACTATTAATACCTTATTTTCCAAAAATATTTGGAAACCCAC 1978
Qy      621 PheAsnArgIleSerLeuLeuGlyLys 629
Db      1979 TTCAATAGGATTTCACTTGTGAAAG 2005

RESULT 3
ID AEA51089 standard; DNA; 2859 BP.
XX AEA51089;
AC
XX
XX
DT 11-AUG-2005 (first entry)
XX
XX
DE Human DNAX cytokine receptor subunit 5 (DCRS5) DNA.
XX
XX Diagnosis; therapeutic; asthma; antiasthmatic; immune disorder;
XX Inflammation; respiratory disease; allergy; anti-allergic;
XX Chronic obstructive pulmonary disease; respiratory-gen.;
XX pulmonary fibrosis; anti-inflammatory; pneumonia; infection;
XX cytokine receptor family; gene; ds.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT 819..peptide 1..187
FT /*tag= a
FT 119..2008
FT /*tag= b
FT /*product= "Human DNAX cytokine receptor subunit 5 (DCRS5)
FT protein"
FT /*transl_except= (pos:125..127, aa: Xaa)
FT /*note= "Xaa corresponds to Gln or His"

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 FT /note= "Xaa corresponds to Gly or Arg"  
 FT mat\_peptide 188..2005  
 FT /\*tag= c  
 FT /product= "Mature human DNAX cytokine receptor subunit 5  
 FT (DCRS5) protein"  
 FT  
 PN W02005052157-A1.  
 PN  
 XX 09-JUN-2005.  
 PD  
 XX  
 XX 18-NOV-2004; 2004MO-US038886.  
 PF  
 XX 21-NOV-2003; 2003US-00720026.  
 PR  
 XX (SCHE ) SCHERING CORP.  
 PA  
 PI Chirica M, Kaetelein RA, Moore KW, Parham CL;  
 XX WPI; 2005-41800/42.  
 XX P-PDB; AEA51090.  
 DR  
 XX  
 XX  
 PT Use of an agonist or antagonist of DNAX cytokine receptor subunit 5  
 PT (DCRS5) or of p19 for treating a human subject experiencing a  
 PT physiological disorder such as allergy or chronic obstructive pulmonary  
 PT disorder (COPD).  
 PT  
 XX  
 PS Claim 1; SEQ ID NO 1; 89pp; English.  
 XX  
 XX The present invention relates to a method of treating a human subject  
 CC experiencing a physiological disorder. The method involves administering  
 CC an agonist or antagonist of DNAX cytokine receptor subunit 5 (DCRS5, also  
 CC known as IL-23r) or of p19, where the disorder comprises asthma or  
 CC allergy, chronic obstructive pulmonary disorder (COPD) or an interstitial  
 CC lung disorder. The invention is useful for treating interstitial lung  
 CC disorder e.g. idiopathic pulmonary fibrosis, eosinophilic granuloma and  
 CC hypersensitivity pneumonitis. The present sequence is the human DCRS5  
 CC DNA.  
 CC  
 SQ Sequence 2859 BP; 929 A; 575 C; 560 G; 791 T; 0 U; 4 Other;  
 XX  
 Alignment Scores:  
 Pred. No.: 4..9e-304 Length: 2859  
 Score: 3324.00 Matches: 629  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 99.9% Indels: 0  
 DB: 14 Gaps: 0  
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 DB 119 ATAATATCAKGTCACTATTCATAGGATGAGATGAGATACCCCTTACATACCTCTCAGCTGG 178  
 QY 21 CyHhieg1v61y1leThraen1leAenCySeSerG1yHh1leThrPvAlG1uproAlaThr 40  
 DB 179 TGCATAGGAGAAATTAACAATTAATTAATGCTGCGCAACATCGGATGAACAGCCACA 238  
 QY 41 IlPheIyMeSerG1yMeCaen1leSer1leTyrcySg1na1a1a1leTyraSncySg1n 60  
 DB 239 ATTTTAAAGATGGGTATGATATCTCTATATATTGCCAAGAGAAATTAAGAACTGCGCA 298  
 QY 61 ProArG1yLeuHh1ePheTyrlYvAenG1y1leYsG1uArGpHeG1n1leThraX1le 80  
 DB 299 CCAAGGAACCTCATTTTATAAATAATGATCAAAAGAAATTTCAATCACAAGGATT 358  
 QY 81 AsnLysHh1rThra1aAaG1eUThrTyrlYvAaSnPheLeuG1uproH1sa1aSerMetTyr 100  
 DB 359 AATTAACAACAAGCTCGCTTGATTAATAAATCTTCGAAACCAATGCTCTATATAC 418  
 QY 101 Cyethr1a1aG1uCyvProLySh1ePheG1nG1uThrLeu1leCyvG1yLyAsp1leSer 120

DB 419 TGCATGCTGATGTGCCAAACATTTTCAAGAGACACTGATATGTGAAAAAGACATTTCT 478  
 QY 121 SerG1yTyrcProProAsp1leProAspG1uValThrcyEva1leTyrg1uTyrsG1y 140  
 DB 479 TCTGATATCCGCGAATATTCCTGATGAAGTAACTGATGCTTATATGAATATTCAGGC 538  
 QY 141 AsnMetThrcySthTrThraen1a\*\*\*LyLeuThTyrlleAspHh1yLyTyrlVal 160  
 DB 539 AACATGACTTGCACTCGGAATGCTRGAAGCTCACCATCAATGACAAATAATCGGGTA 598  
 QY 161 H1sValLySerLeuG1uThrG1uG1uG1uG1uG1uG1uG1uG1uG1uG1uG1uG1uG1u 180  
 DB 599 CATGTAAAGATTTAAGACAGAAAGAGCAACATATCTCACTCAAGCTATATTAC 658  
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 QY 201 AlaLeuG1yMeSerG1uSerLySg1uLeuG1n1leH1leuAspAsp1leVal1lePro 220  
 DB 719 GCACTAGGATGGAAAGTCAAAACAACAGCAAAATTCACCTGGATGATATAGTATCT 778  
 QY 221 Ser1a1a1aVal1leSerArG1aG1uThr1leAsnAlaThrValProLySthTr1le 240  
 DB 779 TCTGACCGCTCATTTCCAGGCTGAGACTATTAATGCTACAGTCCCAAGACCATAT 838  
 QY 241 TyrTrpAspSerG1nThrThr1leG1uLyValSerCySg1uMeArG1yLySAlaThr 260  
 DB 839 TATTGGATATGTCAAACAATTAAGATTTCTCTGTAATGATACAAAGCTTCA 898  
 QY 261 ThrAsnG1nThrTrpAsnValLySg1uPheAspThraSnpheThrTyrlValG1nG1nSer 280  
 DB 899 ACAACCAAACTTGAAATGTAAAGATTTGACACCAATTTTCAATATGCAACAGTCA 958  
 QY 281 GluPheTyrlLeuG1uProAsn1leLyTyrlYvAlPheG1nValArG1ySg1nG1uThrG1y 300  
 DB 959 GAATTCCTACTGAGGCAACATTAAGTACGATTTCAAGTGAAGTCAAGAAACGGC 1018  
 QY 301 LyvArG1yTyrlProG1nProTrpSerSerProPheHh1eLySthThrProG1uThrValPro 320  
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 DB 1079 CAGGTACATCAAAACATTCACAAATGACACATGGAATTCGGGCTTAACAGTTGCTTC 1138  
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 DB 1199 ATGCTCTTGCTGTATATGTTGTAATCTTCTTGAATGGATTTTAACAATCATTC 1258  
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 DB 1319 CTTAATATGAAAAACGCAATGTTGTGAATAATCTCAGGAAAAATGTGAATCTTAATCAAT 1378  
 QY 421 AsnAsnSerSerG1uG1nVal1leuTyrlYvAlAspProMet1leThrcy1leYsG1u1le 440  
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 QY 441 Phe1leProG1uHh1eLySProThraAspTyrlYvLySg1uAsnThrcyProLeuG1uThr 460  
 DB 1439 TTTATCCCAAGAACACAAGCTTCAAGCTACAAAGAGAAATACAGAGACCCCTCGAGACA 1498  
 QY 461 ArgAspTyrcProG1nAsnSerLeuPheAspAsnThrThrValValTyrlleProAspLeu 480  
 DB 1499 AGAGACTACCCGAAAACCTCGCTATTCGACAAATACAGTGTATATATATCTCTGATCTC 1558

QY 481 AenThrGlyTyrIleProGlnIleSerAsnPheLeuProGlnIleSerHisLeuSerAsn 500  
 Db 1559 AACACTGATATTAACCCCAATTTCTGCTGAGGAAAGCCATCTCAGCAAT 1618  
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 Db 1619 AATTAAGAAATTAATCTTCTTAACCTTAACCAACAGTTAATCTTAAGCTCAGGAAT 1678  
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 Db 1739 AGCAACACATATTTCTTGAGAGATTAAGCTCATATTAATCAAGAGAAATCAGATTCT 1798  
 QY 561 ProAspIleGlnAsnSerValGlnIleGlnIleThrThrMetLeuLeuGlnAsnAspSerPro 580  
 Db 1799 CCGACATACAAACCTCAGTAGAGAGAAACCAACCTGCTTTGAAATGATCAACC 1858  
 QY 581 SerGlnThrIleProGlnIleThrLeuLeuProAspGlnPheValSerCysLeuGlyIle 600  
 Db 1859 AGTGAACATATTCAGAACAGACCCCTGCTTCTGATGAATTTGCTCTGTTGGGATC 1918  
 QY 601 ValAsnGlnIleLeuProSerIleAsnThrTyrPheProGlnAsnIleLeuGlnIleSerHis 620  
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 QY 621 PheAsnArgIleSerLeuGlnIleGly 629  
 Db 1979 TTCAATAGATTTCACTTGAAGAAAG 2005

## RESULT 4

ADVA3392  
 ID ADVA3392 standard; cDNA; 1890 BP.

AC ADVA3392;

DT 10-MAR-2005 (first entry)

DE Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 1020.

KW microarray; psychoneuroendocrinimmune; chronic fatigue;  
 non-insulin dependent diabetes; allergy; immune disorder; inflammation;  
 cancer; neoplasm; infection; expressed sequence tag; ss.

OS Homo sapiens.

PN W02004108899-A2.

PD 16-DEC-2004.

PF 04-JUN-2004; 2004W0-US017686.

PR 04-JUN-2003; 2003US-0475915P.

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PI Nicholson A, Vernon SD;

DR WPI; 2005-031682/03.

PT New microarray comprising probes for genes involved in  
 psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a  
 condition associated with PNI activity, e.g., inflammatory or infectious  
 diseases.

PS Claim 1; SEQ ID NO 1020; 254bp; English.

CC The invention relates to a new microarray which comprises probes for  
 genes involved in psychoneuroendocrinimmune (PNI) activity. The  
 microarray is useful in diagnosing a condition associated with PNI

CC activity, such as CFS, type-2 diabetes, allergic condition, inflammation,  
 CC cancer and infection. The present sequence represents a  
 CC psychoneuroendocrinimmune gene expressed sequence tag. Note the  
 CC specificatio mentions SEQ ID NO of up to 3314 but only sequences up to  
 CC SEQ ID NO 1829 are provided.

XX Sequence 1890 BP; 647 A; 377 C; 347 G; 519 T; 0 U; 0 Other;

## Alignment Scores:

Score:	2,41e-303	Length:	1890
Percent Similarity:	3314.00	Matches:	626
Best Local Similarity:	99.5%	Conservative:	0
Query Match:	99.6%	Mismatches:	3
DB:	14	Indels:	0
		Gaps:	0

US-10-667-289-2 (1-629) X ADVA3392 (1-1890)

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 Db 361 TCTGATATCCCGCAATATTTCTGTATGAAGAACCTGTGTCAATTAATATCAAGGC 420  
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 Db 481 CATGTGAAGATTTAGAGACAGAAAGAGCAACAGTATCTCACCTCAAGCTATATTAAC 540  
 QY 181 IleSerThrAspSerLeuGlnIleGlyIleValTyrIleValIleTyrValIleAlaAlaAsn 200  
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 QY 201 AlaLeuGlnMetGlnIleSerIleGlnIleGlnIleHisLeuAspAspIleValIlePro 220  
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 Db 661 TCTGACGCCGTATTTCCAGGCTGAGATTAATAGTACAGTGCCAAAGCCATTAAT 720  
 QY 241 TTTTPAspSerGlnThrThrIleGlnIleValSerCysGlnMetCysGlyIleValThr 260  
 Db 721 TATTTGGATATGTCAAACAAATGAAAGGTTTCTCTGGAATGAGATACAGCTACCA 780  
 QY 261 ThrAsnGlnThrThrAsnValIleGlnIlePheAspThrAsnPheThrTyrValGlnIleSer 280  
 Db 781 ACAAACCAACATTTGGAATGTAAAGATTTGAACCAATTTTACATATGTGACAGTCA 840



QY 281 GluPheTyrLeuGluProAsnIleLysTyrValPheGluValArgCysGlnGluThrGly 300  
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 QY 401 ProAsnMetLysAsnSerAsnValValLysMetLeuGlnGluAsnSerGluLeuMetAsn 420  
 DB 1201 CCTAATATGAAACACGAAATGTTGTGAATACTACAGAAATAGTGAATCTTAATGAAT 1260  
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 DB 1261 AATAATTTCCAGTACGAGCGTCTTATGTTGATCCCATGATTACAGAGATTAAGAAATC 1320  
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 QY 461 ArgAspTyrProGluAsnSerLeuPheAspAsnThrThrValValTyrIleProAspLeu 480  
 DB 1381 AGGACATCAACCGCAAACTGCTATTCGACAAATACATCACTGATATATATCTCGATCTC 1440  
 QY 481 AsnThrGlyTyrLysProGlnIleSerAsnPheLeuProGluGlySerHisLeuSerAsn 500  
 DB 1441 AACACGTGGAATTAACCCCAATTTTCAATTTCTGCTGAGGAGAACCTTCAGCAAT 1500  
 QY 501 AsnAsnGluIleThrSerLeuThrLeuLysProProValAspSerLeuAspSerGlyAsn 520  
 DB 1501 AATAATGAATTAATCTTCCTTAACACTTAACCAACAGTTGATTCCTTAAGACTCAGGAAT 1560  
 QY 521 AsnProArgLeuGlnLysHisProAsnPheAlaPheSerValSerSerValAsnSerLeu 540  
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 QY 581 SerGluThrIleProGluGlnThrLeuLeuProAspGluPheValSerCysLeuGlyIle 600  
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 QY 601 ValAsnGluGluLeuProSerIleAsnThrTyrPheProGluAsnIleLeuGluSerHis 620  
 DB 1801 GTGAATGAGAGTTGCGATCTTAATTAATCTTATTTCCAAATAATTTTGGAAAGCCAC 1860  
 QY 621 PheAsnArgIleSerLeuLeuGlyLys 629  
 DB 1861 TTCAATGAGATTCACCTTGAAAG 1887

RESULT 5  
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 ID AAF87822 standard; cDNA; 1910 BP.  
 AC AAF87822;  
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 DT 11-JUL-2001 (first entry)  
 DE Human haemopoietin receptor protein NR12.5 encoding cDNA SEQ ID NO:9.  
 KW Human; haemopoietin receptor protein; NR12; immunosuppressive;  
 KW antiallergic; haemopoietin factor; autoimmune disease; tissue rejection;  
 KW metal allergy; pollen allergy; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 1..1890  
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 FT /product= "NR12.5"  
 FT /note= "haemopoietin receptor protein"  
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 XX MO200123556-A1.  
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 PF 27-SEP-2000; 2000MO-JP006654.  
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 PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.  
 XX  
 PI Maeda M, Yaguchi N;  
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 XX WPI; 2001-266154/27.  
 DR P-PSDB; AAB74967.  
 XX  
 PT New haemopoietin receptor protein NR12 useful for screening for new  
 PT binding factors for potential treatment of autoimmune disease, tissue  
 PT rejection and allergies.  
 XX  
 PS Claim 1; Fig 13; 140pp; Japanese.  
 CC The present sequence encodes a human haemopoietin receptor protein NR12  
 CC designated NR12.5. NR12 has immunosuppressive and antiallergic  
 CC activities. NR12 can be used for searching for haemopoietin factors with  
 CC the potential for controlling autoimmune disease, tissue rejection and  
 CC allergies against e.g. metals and pollen  
 SQ Sequence 1910 BP; 654 A; 379 C; 352 G; 525 T; 0 U; 0 Other;  
 Alignment Scores:  
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 Score: 3314.00 Matches: 626  
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 DB 121 ATTTTAAGATGGGTATGATATATCTCTATATATATGCAAGCAAGCAATTAAGAACTCCAA 180

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 QY 101 CysThrAlaGluCysProLyshisPhegluGluThrleuileCysgllysaaspiIeser 120  
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 QY 121 SerGlyTyProProaspIleProaspGluValThrCysValileTyrglyTyserGly 140  
 Db 361 TCTGGATATCCGCACAGATATTCCTGATGAAGTAACTGTGTCAATTAATGATTCAGGC 420  
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QY 421 AsnAsnSerSerGluGluValleuTyTyValAspProMetCilethrgluileGlyGluile 440  
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 Db 1741 AGTGAACATATTCACAAACAGACCCCTGCTTCGAGAAATTTGTCTCTGTTGGGAGATC 1800  
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 QY 621 PheAsnArgIleSerleuGluGlylyse 629  
 Db 1861 TTCATATGAGATTCACCTTGGAAAAG 1887  
 DE RESULT 6  
 ID AAD38773 standard; cDNA; 2830 BP.  
 AC AAD38773;  
 XX AAD38773;  
 XX 23-SEP-2002 (first entry)  
 DE Human haematopoietin receptor 2 (HPR2) cDNA.  
 XX Human; haematopoietin receptor; receptor; HPR1; HPR2; cell proliferation;  
 XX pancytopenia; leukopenia; anaemia; thrombocytopenia; osteoporosis;  
 XX neurodegenerative disorder; leukemia; carcinoma; haematologic disorder;  
 XX cancer; myeloid dysplastic syndrome; idiopathic thrombocytopenic purpura;  
 XX ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;  
 XX osteoclast disorder; peridontitis; acute polynuropathy; Bell's palsy;  
 XX anorexia nervosa; chronic fatigue syndrome; Creutzfeldt-Jacob disease;  
 XX demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;  
 XX vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;  
 XX stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;  
 XX lechaemic disease; gene; ss.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 XX  
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 FT /note= "this region is specifically claimed as SEQ ID NO:

FT sig\_peptide 20 in claim 9 of the specification"  
 FT 137.175  
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 FT mat\_peptide 176.1993  
 FT /\*tag= c  
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 FT /\*tag= d  
 FT variation replace(2172, g)  
 FT /\*tag= e  
 PN MO200229060-A2.  
 PD 11-APR-2002.  
 PF 05-OCT-2001; 2001MO-US031634.  
 PR 06-OCT-2000; 2000US-0238706P.  
 PR 13-OCT-2000; 2000US-0240476P.  
 PR 20-FEB-2001; 2001US-0270282P.  
 XX (IMM) IMMUNEX CORP.  
 PA Cosman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR;  
 PI P-PSDB; AAE24033.  
 DR WPI: 2002-330172/36.  
 XX P-PSDB; AAE24033.  
 PT Human and murine hematopoietin receptor polypeptides HPR1 and HPR2,  
 PT useful for treating cell proliferation, metabolic, and reproductive  
 PT hormone related conditions.  
 PS Claim 9; Page 117-119; 136pp; English.  
 XX The present invention relates to human and murine hematopoietin receptor  
 CC polypeptides HPR1 and HPR2. Sequences of the invention are useful for  
 CC treating cell proliferation conditions e.g., pancytopenia, leukopenia,  
 CC anaemia, thrombocytopenia, neurodegenerative disorders and osteoporosis  
 CC resulting from a lack of bone-forming cells. They are also useful for  
 CC treating cell proliferation conditions such as leukemia and tumor  
 CC metastasis, osteoporosis resulting from an excess of bone-resorbing  
 CC cells. HPR sequences are also useful for treating medical conditions and  
 CC diseases such as cell proliferation, metabolic and reproductive hormone  
 CC related conditions. They are useful for treating various haematologic and  
 CC oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal  
 CC carcinoma, myelogenous leukemia, colon, stomach, prostate, renal cell,  
 CC cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including  
 CC cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma,  
 CC sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer),  
 CC squamous cell carcinoma), haematologic disorders, anaemias (e.g., anaemia  
 CC of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelo-  
 CC dysplastic syndromes (including refractory anaemia, refractory anaemia  
 CC with ringed sideroblasts or with excess blasts), idiopathic thrombocyto-  
 CC penic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/  
 CC myeloid metaplasia, osteoclast disorders that lead to bone loss such as  
 CC osteoporosis including post-menopausal osteoporosis, periodontitis  
 CC resulting in tooth loosening or loss, prosthesis loosening after joint  
 CC replacement, neurodegenerative conditions (e.g., acute polyneuropathy,  
 CC Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible  
 CC dementia including Creutzfeldt-Jacob disease, demyelinating neuropathy,  
 CC Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome,  
 CC myasthenia gravis, chronic neuronal degeneration, stroke including  
 CC cerebral ischaemic diseases. HPR1 and HPR2 polypeptides are also useful  
 CC for treating various other disorders such as osteoporosis, obesity,  
 CC deficient mammary development and infertility. The present sequence is  
 CC human HPR1 cDNA  
 SO Sequence 2830 BP; 922 A; 574 C; 551 G; 783 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 4.27e-303  
 Score: 3314.00  
 Percent Similarity: 99.5%

Best Local Similarity: 99.5% Mismatches: 3  
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 Db 287 CCAAGGAACCTTCATTTTATTAATAATGGCATCAAGAAAGATTTCAAATCACAAGATT 346  
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QY 621 PheAsnArgIleSerLeuLeuIleValSer 629
DB 1967 TTCAATAGATTTCACTTGGAAAG 1993

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KW metal allergy; pollen allergy; ss.
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XX /note= "haemopoietin receptor protein"
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XX 27-SEP-1999; 99JP-00273358.
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XX 03-AUG-2000; 2000JP-00240397.
XX
XX (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
XX Maeda M, Yaguchi N;
XX WPI; 2001-266154/27.
XX
XX P-PSDB; AAB74965.
XX
XX
XX New hemopoietin receptor protein NR12 useful for screening for new
XX binding factors for potential treatment of autoimmune disease, tissue
XX rejection and allergies.
XX
XX Claim 1; Fig 6; 140pp; Japanese.
XX
XX The present sequence encodes a human haemopoietin receptor protein NR12
XX designated NR12.3. NR12 has immunosuppressive and anti-allergic
XX activities. NR12 can be used for searching for haemopoietin factors with
XX the potential for controlling autoimmune disease, tissue rejection and
XX allergies against e.g. metals and pollen
XX
XX Sequence 2123 BP; 731 A; 419 C; 395 G; 578 T; 0 U; 0 Other;
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XX
XX 61 ProArgLysLeuHisPheTyrLysAsnGlyIleLysGlyLysArgPheGlnIleThrArgIle 80
XX 278 CCAAGAAATCTCATTTTATTAATAATGGCATCAAGAAAGATTTCAATCAAGGATT 337
XX
XX 81 AsnLysThrThrAlaArgLeuTyrTyrLysAsnPheLeuGlyProHisAlaSerMetTyr 100
XX 338 AATTAACAAACAGCTGGCTTGGTATTAATAAATCTTCTGGAACCAATGCTTATGTAC 397
XX
XX 101 CysThrAlaGlyCysProLysHisPheGlnGlnThrLeuIleCysGlyLysAspIleSer 120
XX 398 TGCACCTGGAATGTCCAAACATTTTCAAGAGACCTGATATGTGAAAAAGCATTTCT 457
DB

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PI Cosman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR,  
 XX WPI; 2002-330172/36.  
 DR P-PSDB; AAE24034.  
 XX  
 PT Human and murine hematopoietin receptor polypeptides HPR1 and HPR2,  
 PT useful for treating cell proliferation, metabolic, and reproductive  
 PT hormone related conditions.  
 XX  
 PS Claim 9; Page 123-124; 136pp; English.  
 XX  
 CC The present invention relates to human and murine hematopoietin receptor  
 CC polypeptides HPR1 and HPR2. Sequences of the invention are useful for  
 CC treating cell proliferation conditions e.g., pancytopenia, leukopenia,  
 CC anaemia, thrombocytopenia, neurodegenerative disorders and osteoporosis  
 CC resulting from a lack of bone-forming cells. They are also useful for  
 CC treating cell proliferation conditions such as leukemia and tumor  
 CC metastasis, osteoporosis resulting from an excess of bone-resorbing  
 CC cells. HPR sequences are also useful for treating medical conditions and  
 CC diseases such as cell proliferation, metabolic and reproductive hormone  
 CC related conditions. They are useful for treating various hematologic and  
 CC oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal  
 CC carcinoma, myelogenous leukemia, colon, stomach, prostate, renal cell,  
 CC cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including  
 CC cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma,  
 CC sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer),  
 CC squamous cell carcinoma), haematologic disorders, anaemias (e.g., anaemia  
 CC of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelo-  
 CC dysplastic syndromes (including refractory anaemia, refractory anaemia  
 CC with ringed sideroblasts or with excess blasts), idiopathic thrombocyto-  
 CC penic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/  
 CC myeloid metaplasia, osteoclast disorders that lead to bone loss such as  
 CC osteoporosis including post-menopausal osteoporosis, periodontitis  
 CC resulting in tooth loosening or loss, prosthesis loosening after joint  
 CC replacement, neurodegenerative conditions (e.g., acute polyneuropathy,  
 CC Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible  
 CC dementia including Creutzfeldt-Jacob disease, demyelinating neuropathy,  
 CC Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome,  
 CC myasthenia gravis, chronic neuronal degeneration, stroke including  
 CC cerebral ischaemic diseases. HPR1 and HPR2 polypeptides are also useful  
 CC for treating various other disorders such as osteoporosis, obesity,  
 CC deficient mammary development and infertility. The present sequence is  
 CC human HPR2 ex8-ex9 DNA  
 XX  
 SQ Sequence 1698 BP; 597 A; 335 C; 310 G; 456 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 3,89e-269 Length: 1698  
 Score: 2952.00 Matches: 562  
 Percent Similarity: 89.3% Conservative: 0  
 Best Local Similarity: 89.3% Mismatches: 3  
 Query Match: 88.8% Indels: 64  
 DB: 6 Gaps: 1  
 US-10-667-289-2 (1-629) x AAD36774 (1-1698)  
 QY 1 MetAsn\*\*ValThrIleGlnTPAspAlaValIleAlaLeuTYrIleLeuPheSerTyr 20  
 Db 1 ATGATCAGGTCACTATTCATATGAGATGAGATATATACCCCTTATCATATCTTCAGCTGG 60  
 QY 21 CyeHisGlyGlyIleThrAsnIleAsnCyseSerGlyHisIleTyrValGluProAlaThr 40  
 Db 61 TGCATCGAGAAATTACAAATATATTAATGCTGCGCAATCTGGGAGAACCAAGCCACA 120  
 QY 41 IlePheIleMetGlyMetAsnIleSerIleTyrCyseGlnAlaIleIleIleAsnCyseGln 60  
 Db 121 ATTTTAAAGATGGATGAATATCTCTATATATTCAGAGAGCAATTAAGAACTGCAA 180  
 QY 61 ProArgIleLeuHisPheTYrIleAsnGlyIleIleGluIleArgPheGlnIleThrArgIle 80  
 Db 181 CCAAGGAAATCTTATTTTATTAATAAATGCGATCAAAAGAAATTTCAAAATCAAGAGATT 240  
 QY 81 AsnIleThrThrAlaArgLeuTyrTYrIleAsnPheLeuGluProHisAlaSerMetTyr 100

Db 241 AATAAAAACAACACCTGGCTTGGTATAAAAATTTCTGGAAACACACCTTCTAATGATAC 300  
 QY 101 CyeThrAlaGluCyseProIleHisPheGlnGluThrLeuIleCyseGlyIleAspIleSer 120  
 Db 301 TGCACTCGTGAATATGTCACAAACATTTTCAAGAGACACTGATATGTGAAAAAGCATTTCT 360  
 QY 121 SerGlyTYrProProAspIleProAspGluValThrCyseValIleTyrGluTyrSerGly 140  
 Db 361 TCTGATATCCCGCAGATATTCCTGATGAAGTAACCTGTGTCTATTTATGATATTCAGGC 420  
 QY 141 AsnMetThrCyseThrThrPheAsnAla\*\*\*IleLeuThrTYrIleAspThrIleTyrValIle 160  
 Db 421 AACATACCTTGACCTCGGAATGTGGGAAGCTCCTACCTACATACACAAATACGTGGTA 480  
 QY 161 HisValIleSerLeuGluThrGluGluGluGlnGlnIleTyrLeuThrSerSerTyrIleAsn 180  
 Db 481 CATGTGAAGAGTTTAAAGACAGAAAGAGCAACATATCTCCCTCAAGCTATATTAAAC 540  
 QY 181 IleSerThrAspSerLeuGlnGlyGlyIleIleValIleValIleValIleValIleValIle 200  
 Db 541 ATCTCCACATGATTCATTACAGAGTGCGCAAGTAAGTCTGTGGGTCCAGACGCAAAAC 600  
 QY 201 AlaLeuGlyMetGluGluIleSerIleGluGlnIleHisIleAsnAspAspIleValIlePro 220  
 Db 601 GCACTAGGACATGGAAAGATCAAAACATGCAAAATTCACCTGATATATATGATACCT 660  
 QY 221 SerAlaAlaValIleSerArgAlaGluThrIleAsnAlaThrValProIleThrIleIle 240  
 Db 661 TCTGCAAGCCGTCAATTTCCAGGCGTGAGACATTAATAGCTACAGTCCAAAGACATTAAT 720  
 QY 241 TYrTyrAspSerGlnThrIleGluIleValIleSerCyseGluMetArgTYrIleValIleThr 260  
 Db 721 TATTTGGATATGTAACAAACAAATTTGAAAGTTTCTGTGAATATGATACCAAGGCTTACA 780  
 QY 261 ThrAsnGlnThrThrAsnValIleValIleValIleValIleValIleValIleValIleValIle 280  
 Db 781 ACAAAACCAACCTTGAATGTAAAGAAATTTGACCAAAATTTTCAATATGCAACAGTCA 840  
 QY 281 GluPheTyrLeuGluProAsnIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 300  
 Db 841 GAATTTCTACTGAGCGCAACCAATTAAGTACGTAATTTCAAGTGAAGTCAAGAAACAGCG 960  
 QY 301 ILeArgTYrTyrGlnProIleProIleSerSerProPhePheHisIleIleIleIleIleIleIle 320  
 Db 901 AAAAGTACTGCGACGCTTGAAGTTTCTGATTTTTCATATAAACACCTGAA----- 951  
 QY 321 GlnValThrSerIleAlaPheGlnHisAspThrTyrAsnSerGlyLeuThrValAlaSer 340  
 Db 951 ----- 951  
 QY 341 IleSerThrGlyHisIleuThrSerAspAsnArgGlyAspIleGlyLeuLeuLeuGlyMet 360  
 Db 951 ----- 951  
 QY 361 IleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380  
 Db 951 ----- 951  
 QY 381 ArgThrGlyIleIleAspArgGlyIleLeuLeuLeuIleProIleTyrPheLeuTYrGluAspIle 400  
 Db 952 ---ACAGGATTAAGAAAGAGATCTTATGTTATATCAAAAGTGGCTTTATGAAAGATTT 1008  
 QY 401 ProAsnMetIleAsnSerAsnValIleValIleMetLeuGlnIleAsnSerGluLeuMetAsn 420  
 Db 1009 CTTAATATGAAAAACGCAATGTTTGAAAAATCTCAAGAAAAATAGTGAATCTTAATGAAT 1068  
 QY 421 AsnAsnSerSerGluGlnValIleIleValIleAspProMetIleThrGluIleIleGluIle 440  
 Db 1069 AATTAATTCAGTAGAGAGGCTTATATGTGATCCCATGATTAACAAGATTAAGAAATTC 1128  
 QY 441 PheIleProGluHisIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 1188  
 Db 441 PheIleProGluHisIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 1248



Db 1129 TTCATCCAGACAGACAGCTACAGTACAGAGAGAGATACAGAGCCCTGAGACA 1188  
Qy ArgAspThrProGlnSerLeuPheAspAsnThrValValIleProAspLeu 480  
Db 1189 AGAGACTACCCGCAAACTGCTATTCAGCAATACATGATTAATATTCCTGATCTC 1248  
Qy AsnThrGlyTyrIysProGlnIleSerAsnPheLeuProGlnIleSerHisLeuSerAsn 500  
Db 1249 AACGACGATATTAACCCCAATTTTCTGCTGAGGAGCCATCTCAGCAAT 1308  
Qy AsnAsnGlnIleThrSerLeuThrLeuLysProProValAspSerLeuAspSerGlyAsn 520  
Db 1309 AATATGAAATATCTCTTAACCTTAACCACTTAATGATTCCTTAAGACTCAGCAAT 1368  
Qy AsnProArgLeuGlnLysHisProAsnPheAlaPheSerValSerSerValAsnSerLeu 540  
Db 1369 AATCCCGGTACCAAAAGCATCCATATTTGCTTTTCATGTTGGAATTCACATA 1428  
Qy SerAsnThrIlePheLeuGlyGluLeuSerLeuIleLeuAsnGlnIleGlyLysSerSer 560  
Db 1429 AGCAACCAATATTTCTTGAGAGATTAAGCTCATATTAATCAAGAGAAATGCAATTC 1488  
Qy ProAspIleGlnAsnSerValGluGluGluThrThrMetLeuLeuGlnAsnAspSerPro 580  
Db 1489 CCGACATACAAAACCTCAGTACAGAGAGAAACCACTGCTTTGGAAAATGATTCACCC 1548  
Qy SerGluThrIleProGlnGlnThrLeuLeuProAspGluPheValSerCysLeuGlyIle 600  
Db 1549 AGTGAACCTATTCAGAACAGACCCCTCTCCGATGAATTTGCTCTGTTGGGATC 1608  
Qy ValAsnGluGluLeuProSerIleAsnThrTyrPheProGlnAsnIleLeuGlnSerHis 620  
Db 1609 GTGATGAGAGGTGGCATTATTAATCTTAATTTTCCACAAATATTTGGAAAGCCAC 1668  
Qy PheAsnArgIleSerLeuLeuGluLys 629  
Db 1669 TTCATGATTTCACTCTTGAAAG 1695  
RESULT 9  
AAK98258  
ID AAK98258 standard; DNA; 1887 BP.  
XX  
AC AAK98258;  
XX  
DT 28-MAY-2002 (first entry)  
XX  
DE Human DNA cytokine receptor subunit 5 (DCRS5) reverse translation DNA.  
XX  
KW Human; DNA cytokine receptor subunit 5; DCRS5; IL30 receptor;  
KW Immune response; DCRS; p40/IL-130 ligand; cell physiology modulation;  
KW cell development; modulation; TH1-mediated disease; multiple sclerosis;  
KW rheumatoid arthritis; osteoarthritis; inflammatory Bowel disease;  
KW diabetes; psoriasis; sepsis; allergic transplants; recipient;  
KW TH2 response; tumour; viral growth; fungal growth; vaccine;  
KW allergic response; ss; reverse translation.  
XX  
OS Homo sapiens.  
XX  
PN WO200185790-A2.  
XX  
PD 15-NOV-2001.  
XX  
PF 10-MAY-2001; 2001WO-US015057.  
XX  
PR 10-MAY-2000; 2000US-0203426P.  
XX  
PA (SCHE) SCHERING CORP.  
XX  
PI Chirica M, Kastelein RA, Moore KW, Parham CL;  
XX WPI; 2002-062238/08.  
XX  
PT Novel DNA cytokine receptor subunit 5 polypeptide which is subunit of

PT receptor complex for p40/IL-130, useful for treating conditions  
PT associated with abnormal expression or triggering of response to p40/IL-  
PT B30 ligand.  
XX  
PS Disclosure, Page 13; 74pp; English.  
XX  
The present DNA sequence represents a reverse translation of the human  
CC DNA cytokine receptor subunit 5 (defined as DCRS5 or IL30 receptor) of  
CC the invention. DCRS5 is a member of the class I branch of the cytokine  
CC receptor superfamily and is closely related to the IL-6 receptor subunit  
CC gp130 and the IL-12R-Beta-2 subunit. Cytokines are soluble molecules  
CC which play a critical role in controlling the complex cellular  
CC interactions of the immune response. The invention comprises novel  
CC receptors related to cytokine receptors designated DNA cytokine receptor  
CC subunits (DCRS). Specifically the invention comprises a subunit (DCRS5)  
CC for a receptor complex for the p40/IL-130 ligand. The DCRS proteins of  
CC the invention are useful for treating diseases or disorders associated  
CC with abnormal expression or abnormal triggering of response to the p40/IL-  
CC -B30 ligand. The proteins of the invention can be used to modulate the  
CC physiology or development of a cell from a host which exhibits TH-  
CC mediated disease; multiple sclerosis; rheumatoid arthritis;  
CC osteoarthritis; inflammatory bowel disease; diabetes; psoriasis; sepsis;  
CC an allogeneic transplant recipient; chronic TH2 response; tumour; viral or  
CC fungal growth; vaccine recipient; or an allergic response  
XX  
SQ Sequence 1887 BP; 421 A; 183 C; 245 G; 257 T; 0 U; 781 Other;  
Alignment Scores:  
Pred. No.: 1,16e-249 Length: 1887  
Score: 2747.00 Matches: 505  
Percent Similarity: 80.3% Conservative: 0  
Best Local Similarity: 80.3% Mismatches: 124  
Query Match: 82.6% Indels: 0  
DB: Gaps: 0  
US-10-667-289-2 (1-629) x AAK98258 (1-1887)  
Qy 1 MetAsn\*\*\*ValThrIleGlnThrPheAlaValIleAlaLeuThrIleLeuPheSerTyr 20  
Db 1 ATGAACAYGTNACNATHCARTGGAGCGNATNAGCTNTTATATHTYNTTYSSTGG 60  
Qy 21 CysHisGlyGlyIleThrAsnIleAsnCysSerGlyHisIleTyrValGluProAlaThr 40  
Db 61 TGTCAYGNGNATNATHCNAATTAATTAATGATGWSNGNCAVATHTGGGNGARCCNGNACN 120  
Qy 41 IlePheLysMetGlyMetCAsnIleSerIleTyrCysGlnAlaAlaIleLysAsnCysGln 60  
Db 121 ATHTTAARATGGGATGAATGAATATHTSNATHTATGTCARCCNGCNATHAARAAYTGYCAR 180  
Qy 61 ProArgLysLeuHisPheTyrLysAsnGlyIleLysGluLysArgPheGlnIleThrArgIle 80  
Db 181 CCNMGNAARATNCAATTTTATTAARAAYGATTAAGARAGNTTTCARATACNMGNATH 240  
Qy 81 AsnLysThrThrAlaArgLeuTyrTyrLysAsnPheLeuGluProHisAlaSerMetTyr 100  
Db 241 AATTAARAACNACNCGMGNATNTGTTAARAATTTTNTGARCCNACNCGMGNATGTAY 300  
Qy 101 CysThrAlaGluCysProLysHisPheGlnGluThrLeuIleCysGlyLysAspIleSer 120  
Db 301 TGYACNGCNGARTGTCNARCAVTTTCARGARACATVNTATHTGCGNARGAATHTMSN 360  
Qy 121 SerGlyTyrProProAspIleProAspGluValThrCysValIleTyrGlyTyrSerGly 140  
Db 361 WSNNGNTATCCNCCNAGATVATHCNAGATNACNATGATNTATHTATGATATWSNGN 420  
Qy 141 AsnMetThrCysThrTyrAsnAla\*\*\*LysLeuThrTyrIleAspThrLysValVal 160  
Db 421 AATATGACNTGACNTGGAAYGCMGNAARATTAACATTAATTAAGAACAAATATGATGNT 480  
Qy 161 HisValLysSerLeuGlnThrGluGluGlnGlnTyrLeuThrSerSerTyrIleAsn 180  
Db 481 CAYGTNAARWSNTYNGARACNGARGARCARCATTAATTAATCAACNWSNNTATTAATTAAY 540

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Qy 181 ILeSerThraPserLeuGInGlyGlyLeuValThrValAlaAlaAsn 200
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Db 541 ATMSNAACNAYMSNTYTCARGGGAGNAAPAAATAYTNGTGGTCARGGCCNAAY 600
Qy 201 AlaleuGlyMetGluGlySerLeuGlnLeuGlnIleIleuAspPrlIleValPro 220
    |||||
Db 601 GCNTTNGGNAATGGARAGMSNAACARNTTCARATHCATYTTNGAYGATHTGNATCCN 660
Qy 221 SerIleAlaValIleSerArgAlaGluThrIleAsnAlaThrValProLeuThrIle 240
    |||||
Db 661 MSNGCNCNGTNAHTMSMGCGAGARACNAATHAAYCNCNCGTNCNNAARACNAATHA 720
Qy 241 TyrTrpAspSerGlnThrIleGluLeuValSerCysGluMetArgIleValThr 260
    |||||
Db 721 TAYTGGGAYMSNCARACNAATGARAAGTMSNTGYGARAGMGNATYAAARGCAACN 780
Qy 261 ThrAsnGlnThrTrpAsnValIleGluPheAspThrAsnPheThrTyrValGlnGlnSer 280
    |||||
Db 781 ACNAAYCARACNTGGAAVGTNAAGARTTGATGACNAAYTTACNTAYGTNCARACMSN 840
Qy 281 GluPheTyrLeuGluProAsnIleLeuTyrValPheGlnValArgCysGlnGluThrGly 300
    |||||
Db 841 GARTTAYTNGARCCNAAYATTAARTATGTTTTCARGTNGMTGTCARAGAACGCGN 900
Qy 301 LysArgTyrTrpGlnProTrpSerSerProPhePheIleuThrProGluThrValPro 320
    |||||
Db 901 AARMGNATAYGGCARCCTGTGMSMSNCNTTYYTTCAYAARACNCGARACGNTCCN 960
Qy 321 GluValThrSerIleValPheGlnIleAspThrTrpAsnSerGlyLeuThrValAlaSer 340
    |||||
Db 961 CAGGTNACNMSNAACGNTTTCACACAGATCAGTAAGTAAGTNGAGTNGTNCNMSN 1020
Qy 341 ILeSerThrGlyIleThrSerAspAsnArgGlyAspIleGlyLeuLeuGluMet 360
    |||||
Db 1021 ATHTMSNACNCGNCAYYTNACMSNGAFAAAMGCGNCAVATHTGCTNTNTNTNTMGNAATG 1080
Qy 361 IleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380
    |||||
Db 1081 ATHTGNTTTCGCGTNAATGYTNMSNATHTYTNMSNTNATHTGGNATHTTAAVYMGMSNTTY 1140
Qy 381 ArgThrGlyIleLeuAspArgGlyLeuLeuLeuIleProLeuTrpLeuTyrGluAspIle 400
    |||||
Db 1141 MGNCNCGNATHTAARMGCMGNATHTYTNNTNATHTCCNNAARTGTNTTAYGARGAATHT 1200
Qy 401 ProAsnMetIleAsnSerAsnValIleValMetLeuGlnIleAsnSerGluLeuMetAsn 420
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Db 1201 CNAAYATGARAARAYMSNAAYGTMTAARATGTTCARAGRAAYMSNGARATYMTAAT 1260
Qy 421 AsnAsnSerSerGluGlnValLeuTyrValAspProMetIleThrGluIleValGluIle 440
    |||||
Db 1261 AAYAAVMSNMSNGARCARGTNTYNTATGTGATGATHCNARATHTAARGARATHT 1320
Qy 441 PheIleProGluIleValSerProThrAspTyrIleValGluAsnThrGlyProLeuGluThr 460
    |||||
Db 1321 TTTATHTCCNARGARCAAYARCCNACGATTAATARAARARAAVACGNCNCTTNGAARCN 1380
Qy 461 ArgAspTyrProGlnIleAsnSerLeuPheAspAsnThrTyrValIleTyrIleProAspLeu 480
    |||||
Db 1381 MGNGAYTAYCNCNARAYMSNTTGTGAYAAVACNACNCGTNGTNTATHTCCNCAAYTN 1440
Qy 481 AsnThrGlyTyrIleProGlnIleSerAsnPheLeuProGluGlySerIleIleuSerAsn 500
    |||||
Db 1441 AAYAACNCGNTAYARCCNARATHTMSNAAYTTTTCNCGNARGCMNCAAYTTMSNAAY 1500
Qy 501 AsnAsnGluIleThrSerLeuThrLeuValProProAlaAspSerLeuAspSerGlyAsn 520
    |||||
Db 1501 AATTAAGARATHTACNMSNTNACNTTNAACCNCCNCGTNGAYMSNTTNGAYMSNGAAAY 1560
Qy 521 AsnProArgLeuGlnIleValSerProAsnPheAlaPheSerValIleSerValIleSerLeu 540
    |||||
Db 1561 AATCCNMGNTTNCARARARCAVCCNAATTTTGCNTTYSNGTMSNMSNGTNAAYMSNTYN 1620
Qy 541 SerAsnThrIlePheLeuGlyGluLeuSerLeuIleLeuAsnGlnGlyGluCysSerSer 560

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Db 1621 MSNAAYACNATHTTNTTNGCNGARCYTNMSNTNATHTNATAYCARCGNGARTCYMSMSN 1680
Qy 561 ProAspIleGlnAsnSerValGluGluGluThrThrMetLeuLeuIleAsnAspSerPro 580
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Db 1681 CCHGATHTCARARAYMSNGTNGARAGARACACACATGTNTTNGARARAYGAYMSNCCN 1740
Qy 581 SerGluThrIleProGluGlnThrLeuLeuProAspGluPheValSerCysLeuGlyIle 600
    |||||
Db 1741 MSNGARACNATHTCCNARGARACACNTNTTCCNCAAGARTTGTGNTMSNTGTNTNGNATHT 1800
Qy 601 ValAsnGluGluLeuProSerIleAsnThrTyrPheProGlnAsnIleLeuGluSerHis 620
    |||||
Db 1801 GTNAAYGARARATTCNMSNATHTAAYACNTATTTCCNCAARAAYATHTTNGARMSNCAY 1860
Qy 621 PheAsnArgIleSerLeuLeuGlyLys 629
    |||||
Db 1861 TTTAATMGNATHTMSNTTNTTNGARAR 1887

RESULT 10
AAD38777 standard; DNA; 1935 BP.
ID AAD38777;
AC AAD38777;
XX
XX 23-SEP-2002 (first entry)
DT
XX
XX Mouse haematopoietin receptor 2 (HPR2) DNA.
DE
XX
XX Mouse; haematopoietin receptor; receptor; HPR1, HPR2; cell proliferation;
XX pancytopenia; leukopenia; anaemia; thrombocytopenia; osteoporosis;
XX neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder;
XX cancer; myelodysplastic syndrome; idiopathic thrombocytopenic purpura;
XX ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;
XX osteoclast disorder; periodontitis; acute polymyopathy; Bell's palsy;
XX anorexia nervosa; chronic fatigue syndrome; Creutzfeldt-Jacob disease;
XX demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;
XX vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;
XX stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;
XX ischaemic disease; gene; ds.
XX
XX Mus musculue.
OS
XX
XX Key Location/Qualifiers
FH 1.1935
FT CDS /*tag= a
FT /product= "Mouse HPR2 protein"
FT
XX
XX MO200229060-A2.
FN
XX
XX 11-APR-2002.
PD
XX
XX 05-OCT-2001; 2001MO-US031634.
PF
XX
XX 06-OCT-2000; 2000US-0238706P.
PR 13-OCT-2000; 2000US-0240476P.
PR 20-FEB-2001; 2001US-0270282P.
XX
XX (IMMUNEX CORP.
PA
XX
XX Cosman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR;
XX
XX WPI; 2002-330172/36.
DR P-PSDB; AAB24038.
XX
XX Human and murine haematopoietin receptor polypeptides HPR1 and HPR2,
XX useful for treating cell proliferation, metabolic, and reproductive
XX hormone related conditions.
XX
XX Claim 9, Page 135-136; 136pp; English.
XX
XX The present invention relates to human and murine haematopoietin receptor
XX polypeptides HPR1 and HPR2. Sequences of the invention are useful for

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treating cell proliferation conditions e.g., pancytopenia, leukopenia, anaemia, thrombocytopaenia, neurodegenerative disorders and osteoporosis resulting from a lack of bone-forming cells. They are also useful for treating cell proliferation conditions such as leukemia and tumour metastasis, osteoporosis resulting from an excess of bone-resorbing cells. HPR sequences are also useful for treating medical conditions and diseases such as cell proliferation, metabolic and reproductive hormone related conditions. They are useful for treating various haematologic and oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell, cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma, sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer), squamous cell carcinoma), haematologic disorders, anaemias (e.g., anaemia of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelodysplastic syndromes (including refractory anaemia, refractory anaemia with ringed sideroblasts or with excess blasts), idiopathic thrombocytopenic purpura (ITP), sickle cell vasoocclusive crisis, myelofibrosis/myeloid metaplasia, osteoclast disorders that lead to bone loss such as osteoporosis including post-menopausal osteoporosis, peridontitis resulting in tooth loosening or loss, prosthesis loosening after joint replacement, neurodegenerative conditions (e.g., acute polyneuropathy, Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible dementia including Creutzfeldt-Jacob disease, demyelinating neuropathy, Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome, myasthenia gravis, chronic neuronal degeneration, stroke including cerebral ischemic diseases, HPR1 and HPR polypeptides are also useful for treating various other disorders such as osteoporosis, obesity, deficient mammary development and infertility. The present sequence is mouse HPR2 DNA

Sequence 1935 BP; 607 A; 420 C; 385 G; 523 T; 0 U; 0 Other;

Alignment Scores:	
Pred. No.:	1,769-205
Score:	280.50
Percent Similarity:	78.2%
Best Local Similarity:	66.5%
Query Match:	68.6%
DB:	6
	Gaps: 4
	Length: 1938
	Matches: 432
	Conservative: 76
	Mismatch: 115
	Indels: 27

US-10-667-289-2 (1-629) x AAD38777 (1-1935)

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Oy      1 MetAsn***ValThrIleGlnTrpAspAlaValIleAlaLeuTyrlleLeuPheSerTrp 20
Db      1 ATGATGCACTTCACACCTTCAGCTGCATGTGTGTATGACCCCTTATGTGCTTCACAGATGG 60
Oy      21 CysHISGlyGlyIleLeuThrAsnIleAsnCySerGlyPheIleLeuTrpValGlnProAlaThr 40
Db      61 TGTCAAGAGAGAAATCAACAATATAAATCTCTCTGTGACATGTGGGTGTAGCTGTGGTAA 120
Oy      41 IlePheLysMetGlyMetAsnIleSerIleTyryCysGlnAlaIleAlaIleLysAsnCyGln 60
Db      121 ATTTTTCAGATGGGCATTAATGTTTCTTAATATATGTGCAAGAAAGCCCTTAAAGCACTGCCA 180
Oy      61 ProArgLysLeuHisPheTyryLysAsnGlyIleLeuGlnLysPheGlnIleThrArgIle 80
Db      181 CCAAGGAATCTTTACTTTTATAAAAATGGCTTCAAGAAAGAAATTTGATATCAACAAGATT 240
Oy      81 AsnLysThrThrAlaArgLeuTrpTyryLysAsnPheLeuGlnProHisAlaSerMetTyry 100
Db      241 AATAGAACACACAGCTTCGGATTTGGTATAAAGCTTTTCGGAACCTCATGCTTATATGAT 300
Oy      101 CysThrAlaGlnCyPheProLysHisPheGlnGlnThrLeuIleLeuGlySerGlyLysAspIleSer 120
Db      301 TGCACGTGCGAATGTCTCGTCAATTTTCAAGAGACCTGATTTGTGGAAAGACATTTCC 360
Oy      121 SerGlyTyryProProAspIleProAspGlnValThrCysValIleTyryGlyTyrySerGly 140
Db      361 TCTGGAACATCCACCGGATGCCCCCGACCATCTCACATGTCTCATTTTATGAATCTCAGGC 420
Oy      141 AsnMetThrCysThrTrpAsnAla***LysLeuThrTyryIleAspThrLysTyryValVal 160

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Dd	421	AAAGTACATGACCTGGAAACACTGGGAAGCCTACATCATAGATACCAAGTATTGTGG	480
Qy	161	HisVallySerLeuGluThrGluGluGluGlnGlnTyrlLeuThrSerSerTyrlLeuAsn	180
Dd	481	CATGGAAAGAGTTTGGAGACAGAAAGAAACAACAATATCTTGGCTCAAGCTATGTTAAG	540
Qy	181	IlleSerThrAspSerLeuGlnGlyGlyValylsTyrlLeuValITrpValGlnAlaAlaAsn	200
Dd	541	ATCTCCACTGCTCACTGCAGGACGACGAGCAAGTATTGTTGGTGTCCAGCTGTCTCAT	600
Qy	201	AlaLeuGlyMetGluGluSerTyrlLeuGlnIleHisleuAspAspIleValIlePro	220
Dd	601	TCCCTAGGCAATGAGAACTCAACAACAATCAACGCTCATCTGATGATATAGTGAATCT	660
Qy	221	SerAlaValIleSerArgAlaGluThrIleAsnAlaThrValProIysThrIleIle	240
Dd	661	TCTGGTCCATCATTTTCCAGGGCTGAGAGCTACAAACGATACTGTATCCCAAGCATTAGT	720
Qy	241	TyrTrpAspSerGlnThrThrIleGluValSerCySGluMetArgTyrlValAlaThr	260
Dd	721	TACTGAAAAGCAAAACATGATATTGAGAAAGTATTCTGTGAGATGAGATACAAAACA	780
Qy	261	ThrAsnGlnThrTrpAsnValylsGluLysPheAspThrAsnPheThrTyrlValGlnIle	280
Dd	781	ACAAACCAAAAGTGAAGTGTAAAGAAATTTGACGCCAATTTCCATATGATACAGACAT	840
Qy	281	GluPheTyrlLeuGluLysProAsnIleIleTyrlValPheGlnValArgCys-----	296
Dd	841	GAATTTCTACCTCGAGCCAGACAGACAGCAAGTATATATTTCAGTGCATATGCAGAAACT	900
Qy	297	-----GlnGluThrGly	300
Dd	901	AAAAGAACTGGCAGCCTTGAGATTCCCTTTGCCACCAACTTCCCAAGAACTGGT	960
Qy	301	LysArgTyrlTrpGlnProTrpSerSerProPhePheHislystrProGluThrValIlePro	320
Dd	961	AAAAGAACTGGCAGCCTTGAGATTCCCTTTGCCACCAACTTCCCAAGCACTTTC	1020
Qy	321	GlnValThrSerIlyValPheGlnHisAspThrTrpAsnSerGlyLeuThrValAlaSer	340
Dd	1021	CAGGTTACGCAAAATCA--TCCACAGAACTCAGAAAGATGAGATCTCAAGTCTCA	1077
Qy	341	IleSerThrGlyHisLeuThrSerAspAsnArgGlyAspIleGlyLeuLeuLeuGlyMet	360
Dd	1078	ATCTTCAGAGACATCTCGCTTCAGGATATCATCAAGCATTTGGACTTTTCCGGAAATG	1133
Qy	361	IleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe	380
Dd	1138	GTCCTCTTGGCCATCATGATGTGCCATTTTCTCTGATTGGGATATTAAACAGATCACTT	1197
Qy	381	ArgThrGlyIleLysArgArgIleLeuLeuLeuIleProIysTrpLeuTyrlGluAspIle	400
Dd	1198	CGAATAGAGATTTAAAGAAAGATTACTGATGATATCCAAAGATGACTTTATGAAGATATT	1255
Qy	401	ProAsnMetLysAsnSerAsnValValLysMetLeuGlnGluAsnSerGluLeuMetAsn	420
Dd	1258	CTTAATATGAAATATGCAATGTTGGCAAAATATTATACAGGAAAAAGCTATTTGAGAAAT	1317
Qy	421	AsnAsnSerSerGluGlnValLeuTyrlValAspProMetIleThrGluIleLysGluIle	440
Dd	1318	GATATATCCAGTGAAGAGCCCTGTATGTGATCTCTGCTTACAGAGATATAGGAATTC	1377
Qy	441	PheIleProGluHislystrProThrAspTyrlLysGluAsn---ThrGlyProLeuGlu	459
Dd	1378	TCTCCCTCGAACAACAAACCAACGATTTACAAAGAAAGAGCTCACAGGACTCCTTGAG	1437
Qy	460	ThrArgAspTyrlProGlnAsnSerLeuPheAspAsnThrThrValIlyrlIleProAsp	479
Dd	1438	ACAAGAGACTGTCTCTACAGAAATGTTGTCTACAGATTCTTCTGTGTGTATATCTGCAC	1497
Qy	480	LeuAsnThrGlyTyrlLysProGlnIleSerAsnPheLeuProGluGlySerHisLeuSer	499
Dd	1498	CTCAACACTGGATTCAAACCCAGATTTCAAAATCTCTCTCTGGAGAAACCTTTTCATT	1557





QY 281 GluPheTyrLeuGluProAsnIleLysTyrValPheGlnValArgCysGlnGluThrGly 300  
 Db 938 GAATTTACTGAGCCAAACATTAAGTAGTATTTCAAGTAGATGTCAAGAAACAGGC 997  
 QY 301 LysArgTyrTrpGlnProTyrPserSerProPhePheIleuTyrThrProGluThrValPro 320  
 Db 998 AAAAGGTACTGGCGCCCTTGGAGTTCACGTGTTTTCATAAACACCTGAACAGTTCCTCC 1057  
 QY 321 GlnValThrSerLysAlaPheGlnHisAspThrTrpAsnSerGlyLeuThrValAlaSer 340  
 Db 1058 CAGGTCACTCAAAAGCATTCACACATGACACATGCAATTCCTGGCTTACAGTTGCTTCC 1117  
 QY 341 IleSerThrGlyHisLeuThrSerAspAsnArgGlyValIleGlyLeuLeuLeuGlyMet 360  
 Db 1118 ATCTCTACAGGGCACCCTTACTTCTGACACAGAGACATTTGACCTTTATTGGGATG 1177  
 QY 361 IleValIleAlaValIleMetLeuSerIleLeuSerIleuIleGlyIlePheAsnArgSerPhe 380  
 Db 1178 ATCTCTTGTCTGTATGATGTGTCAATCTTCTTGTGATGGATATTTAACAGATCATTC 1237  
 QY 381 ArgThrGlyIleLysArgArgIleLeuLeuLeuIleProLysTrpLeuTyrGluAspIle 400  
 Db 1238 CGAAGTGGAGTTAAAGAGATCTTATTTGTTATACCAAGTGGCTTTATGAAGATATT 1297  
 QY 401 ProAsnMetLysAsnSerAsnValValIleMetLeuGln 413  
 Db 1298 CCTAATATGAAAAACAGCAATGTTGTGAATAATGCTACAG 1336

RESULT 13  
 AAC88149 ID AAC88149 standard; cDNA; 1155 BP.  
 XX AAC88149;

DT 13-MAR-2001 (first entry)

DE Human DNAX cytokine receptor subunit-2 encoding cDNA SEQ ID NO:1.

XX Human; DNAX cytokine receptor subunit; DCRS2; receptor protein;

KW modulating cell proliferation; diagnosis; detection; drug screening;

KM Immunological disorder; ss.

OS Homo sapiens.

XX WO200073451-A1.

PN 07-DEC-2000.

XX 30-MAY-2000; 2000WO-US014867.

XX 01-JUN-1999; 99US-00322913.

XX (SCHER) SCHERING CORP.

XX Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan FJ;

XX WPI; 2001-061536/07.

XX P-PSDB; AAB36646.

PT Novel composition comprising DNAX cytokine receptor subunit polypeptide

XX immunological disorders.

XX Claim 16; Page 10-11; 93pp; English.

XX The present invention describes a composition (I) comprising a  
 CC recombinant DNAX cytokine receptor subunit-2 (DCRS2) polypeptide. The  
 CC DCRS2 polypeptide is useful for binding ligands and for preparing  
 CC antibodies. The DCRS2 polypeptide is also useful for modulating cell  
 CC proliferation, for diagnostic and therapeutic applications, for detecting  
 CC presence of their ligands and in drug screening assays. It is also useful  
 CC for treating conditions such as immunological disorders. The present

CC sequence encodes the human DCRS2 protein

XX Sequence 1155 BP; 387 A; 233 C; 223 G; 312 T; 0 U; 0 Other;

SQ

Alignment Scores:

Pred. No.:	6,19e-183	Length:	1155
Score:	2039.00	Matches:	382
Percent Similarity:	99.2%	Conservative:	0
Best Local Similarity:	99.2%	Mismatches:	2
Query Match:	61.3%	Indels:	1
DB:	4	Gaps:	0

US-10-667-289-2 (1-629) x AAC88149 (1-1155)

QY 1 MetAsn\*\*\*ValThrIleGlnTrpAspAlaValIleAlaLeuTyrIleLeuPheSerTrp 20  
 Db 1 ATGATACAGGTCACTATTTCAATGGAGTGAATAGCCCTTTACATATCTTCACTGAG 60  
 QY 21 CysHISGLYGLYIleThrAsnIleAsnCysSerGlyHisIleTrpValGluProAlaThr 40  
 Db 61 TGTCAATGAGGAATTAATAATATAAATCTGCTGGCCACATCTGGGTAGAACAGCCACA 120  
 QY 41 IlePheLysMetGlyMetAsnIleSerIleTyrCysGlnAlaAlaIleLysAsnCysGln 60  
 Db 121 ATTTTAAGATGGGTATGAATATCTCTATATATTCGCAAGCACAAATTAGAACTGCCAA 180  
 QY 61 ProArgLysLeuHisPheTyrLysAsnGlyIleLysGluArgPheGlnIleThrArgIle 80  
 Db 181 CCAAGGAACCTTATTTTATATAAATGGCATCAAGGAAGAAATTCATATCACAGAGATT 240  
 QY 81 AsnLysThrThrAlaArgLeuTyrTyrLysAsnPheLeuGluProHisAlaSerMetTyr 100  
 Db 241 AATATAACAACAGCTGGCTTGTGTATTAACCTTCTGGAACACATGCTTCTATGTAC 300  
 QY 101 CysThrAlaGluCysProLysHisPheGlnGluThrLeuIleCysGlyLysAspIleSer 120  
 Db 301 TGCATGCTGAAATGTCACCAACATTTTCAGAGACCTGATATGTGAAAAGCATTTCT 360  
 QY 121 SerGlyTyrProProAspIleProAspGluValThrCysValIleTyrGluTyrSerGly 140  
 Db 361 TCTGGATATCGGCAATATCTCTGATGAAGTAACCTGTGTCAATTTATGAAATTCAGGC 420  
 QY 141 AsnMetThrCysThrTrpAsnAla\*\*\*LysLeuThrTyrIleAspThrLysTyrValIle 160  
 Db 421 AACATGACTTGACCTGGAAATGCTGGAGCTCACCTACATACACAAATAATCGGTGA 480  
 QY 161 HisValLysSerLeuGluThrGluGluGluGlnGluGlnIleThrSerSerTyrIleAsn 180  
 Db 481 CATGTGAAGGTTTAGAGACAGAAAGAACCAAGTATCTCACCTCAGACTATATTAC 540  
 QY 181 IleSerThrAspSerLeuGlnGlyLysTyrTyrLeuValTrpValGlnAlaAsn 200  
 Db 541 ATCTCCACTGATTCATTACAAAGCGGCAAGAAATACCTGTTGGTCCAGACAGCAAC 600  
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 Db 601 GCACTAGGCATGGAAGATCAAAACAACTGCAAAATTCACCTGATATATAGATACCT 660  
 QY 221 SerAlaAlaValIleSerArgAlaGluThrIleAsnAlaThrValProLysThrIleIle 240  
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 QY 241 TyrTrpAspSerGlnThrTrpIleGluLysValSerCysGluMetCysArgTyrValAlaThr 260  
 Db 721 TATTTGGATAGTCAACACAAATTGAAGAGTTTCTCTGTGAATATGATCAAGGCTACA 780  
 QY 261 ThrAsnGlnThrTrpAsnValLysGluPheAspThrAsnPheThrTyrValGlnGlnSer 280  
 Db 781 ACAACCAAACTGGAGATGTTAAAGAAATTGACACCAATTTTCAATATGTCAGCAAGTCA 840  
 QY 281 GluPheTyrLeuGluProAsnIleLysTyrValPheGlnValArgCysGlnGluThrGly 300  
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Db      661  TCTGCAACCCGTCATTTCCAGGCGCTGAGACATTAATGCTACAGGCCCAAGACCATATATT 720
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Db      721  TATTGGATGTGCTAAACACATTTGAAAGGTTTCTGTGAATGAGATTCACAGGCTACA 780
Qy      261  ThrAsnGlnThrThrAsnValLysGluPheAspThrAsnPheThrTyValGlnGlnSer 280
Db      781  ACAACCAAACTGGATGTTAAAGATTTGACCCAACTTTTACATATGTCACACGCTCA 840
Qy      281  GluPheTyLeuGluProAsnLysTyValPheGlnValArgCysGlnGlnThrGly 300
Db      841  GAATTCCTACCTGGGCGCAACATTAACTAGTATTTCAAGTGAATGCTCAAGAAACAGGC 900
Qy      301  LysArgTyTrpGlnProPheSerSerProPhePheHisLysThrProGluThrValPro 320
Db      901  AAAAGGTACTGGCGAGCTTGAGTTCCAGTTTCCATTAACACCTGAAACAGTTCC 960
Qy      321  GlnValThrSerLysAlaPheGlnHisAspThrTrpAsnSerGlyLeuThrValAlaSer 340
Db      961  CAGGTCAATCAAAAAGCATTCACACATGACACATGGAATTCGGGCTTACAGTTGCTTCC 1020
Qy      341  IleSerThrGlyHisLeuThrSerAspAsnArgGlyAspIleGlyLeuLeuLeuMet 360
Db      1021  ATCTCTACAGGCGCACTTACTTCTGACACAGAGAGACATTTGACTTTATTTGGGATG 1080
Qy      361  IleValPheAlaValMetLeuSerLysLeuSerLeuIleGlyIlePheAsnArgSerPhe 380
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Qy      381  -ArgThrGlyIle 384
Db      1141  CCGAAGCTGGGATT 1153

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RESULT 15

AD265011 ID AD265011 standard; DNA; 1155 BP.

AC AD265011;

XX 28-JUL-2005 (first entry)

DE DNAX cytokine receptor subunit 2 (DCRS2) DNA, seq id 1.

XX Immunomodulator; cell growth; DNAX cytokine receptor subunits 2; DCRS2;

KM immune disorder; gene; ds.

XX Primates.

XX Location/Qualifiers

FT Key 1.1155

FT CDS /tag= b

FT /product= "DNAX cytokine receptor subunit 2 (DCRS2)"

FT sig\_peptide 1..69

FT mat\_peptide 70..1152

FT /tag= a

FT /tag= c

FT /product= "Mature DCRS2"

XX US2005106673-A1.

XX 19-MAY-2005.

XX 17-DEC-2004; 2004US-00016106.

XX 01-JUN-1999; 99US-0137159P.

XX 31-MAY-2000; 2000US-00588113.

XX 18-SEP-2002; 2002US-00247463.

XX (SCHE) SCHERING CORP.

PI Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan JF;

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XX  WPI; 2005-365817/37.
DR  P-PSDB; AD265012.
XX  Composition useful for diagnosing or creating immunological disorders,
PT  comprising pure or recombinant DNAX cytokine receptor subunit 2 (DCRS2)
PT  polypeptide or its fusion polypeptide.
XX  Disclosure; SEQ ID NO 1; 42pp; English.
XX  The invention relates to a composition (I) of matter chosen from a
CC  substantially pure or recombinant DNAX cytokine receptor subunit 2
CC  (DCRS2) polypeptide. Further disclosed is a substantially pure or
CC  isolated antigenic DCRS2 polypeptide (II) of (I), a fusion polypeptide
CC  (III) of (I) and a method for modulating (M1) the physiology or
CC  development of a cell or tissue culture cells comprising contacting the
CC  cell with an agonist or antagonist of a mammalian DCRS2. (M1) is useful
CC  for modulating the physiology or development of a cell or tissue culture
CC  cells. (I)-(III) are useful for diagnosing or treating immunological
CC  disorders. The current sequence represents the nucleotide sequence of
CC  DNAX cytokine receptor subunit 2 (DCRS2).
XX
SQ  Sequence 1155 BP; 387 A; 233 C; 223 G; 312 T; 0 U; 0 Other;

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Alignment Scores:

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Pred. No.: 6,19e-183 Length: 1155
Score: 2039.00 Matches: 382
Percent Similarity: 99.2% Conservative: 0
Best Local Similarity: 99.2% Mismatches: 2
Query Match: 61.3% Indels: 1
DB: 14 Gaps: 0

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US-10-667-289-2 (1-629) x AD265011 (1-1155)

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Db      1  ATGAATCAGGTCATTCATTCATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 60
Qy      21  CysHisGlyValIleThrAsnIleAsnCysSerGlyHisIleTrpValGluProAlaThr 40
Db      61  TGTCAATGAGGATTTCAAAATTAATTAATCTGCTGGCAATCTGGGATGAGACCAAGCACA 120
Qy      41  IlePheLysMetGlyMetAsnIleSerIleTyCysGlnAlaAlaIleLysAsnCysGln 60
Db      121  ATTTTAAGATGGGATGATGATATCTATATATATGCAAGCAGCAATTAAGAACTCCCAA 180
Qy      61  ProArgLysLeuHisPheTyLysAsnGlyIleLysGlnAlaPheGlnIleThrArgIle 80
Db      181  CCAAGAACTTCAATTTTATTAATAAATGGCATCAAGAAAGATTTCAATCAAGAGATT 240
Qy      81  AsnLysThrThrAlaArgLeuTrpTyLysAsnPheLeuGluProHisAlaSerMetTy 100
Db      241  AATTAACAACACAGCTGGCTTGTGTATTAATACTTTCTGGAACCAATGCTTCTATGTAC 300
Qy      101  CysThrAlaGluCysProLysHisPheGlnGlnThrLeuIleCysGlyLysAspIleSer 120
Db      301  TGCACGTGTAATGTCCCAAACTTTTCAAGAACACTGATATGTGGAAGAACATTTCT 360
Qy      121  SerGlyTyTrpProProAspIleProAspGluValThrCysValIleTyGluTySerGly 140
Db      361  TCTGATATCCCGCAATATCTCTGATGAAGTAACCTGTGTCTTTATGATATTTCAAGGC 420
Qy      141  AsnMetThrCysThrTrpAsnAla***LysLeuThrTyTrIleAspThrLysTyVal 160
Db      421  AACTATGCTTGCACTCTGGAATGTCTGGAGAGCTCACTACATTAACAACAAATACGTGTA 480
Qy      161  HisValLysSerLeuGlnThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 180
Db      481  CATGTGAAGGTTTAAAGACAGAAAGAACAAAGATATCTCACTCAAGCTATATTAAC 540
Qy      181  IleSerThrAspSerLeuGlnGlyLysLysTyLysValTrpValGlnAlaAsn 200
Db      541  ATCTCACTGATTCATTACAAAGGCGCAAGAACTACTGTGTTGGTTCACAGCAGCAAC 600

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Qy 201 AlaLeuGluWheGluSerLySGlnLeuGlnIleHisLeuAspAspIleValIlePro 220
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Db 661 TCTGCAGCCGCAATTCACAGGCTGAGACTATAAATCTACAGTCCCAAGACCATTAAT 720
Qy 241 TyrTrpAspSerGlnThrIleGluLysValSerCysGluMetArgTyrLysAlaThr 260
Db 721 TATTGGGATAGTCAAACAAATGAAAGGTTTCCTGTGAATGAGATACAAAGCTACA 780
Qy 261 ThrAsnGlnThrTrpAsnValLysGluPheAspThrAsnPheThrTyrValGlnGlnSer 280
Db 781 ACAAAACCAACTTGGAAATGTTAAAGAAATTGACACCAATTTTACATATGTGCACAGTCA 840
Qy 281 GluPheTyrLeuGluProAsnIleLysTyrValPheGlnValArgCysGlnGluThrGly 300
Db 841 GAATTTCTACTTGGAGCCAAACATTAAGTACGTATTTCAAGTGAATGTCAAGAAACAGGC 900
Qy 301 LysArgTyrTrpGlnProTyrSerSerProPhePheHisLysThrProGluThrValPro 320
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Qy 321 GlnValThrSerLysAlaPheGlnHisAspThrTrpAsnSerGlyLeuThrValAlaSer 340
Db 961 CAGGTCAATCAAAAGCAATTCACATGACACATGAAATCTGGGCTTACAGTTGCTTCC 1020
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Qy 361 IleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380
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Qy 381 -ArgThrGlyIle 384
Db 1141 CCGAACTGGGATT 1153
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GenCore version 5.1.9  
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OW protein - nucleic search, using frame\_p2n model.

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(without alignments)  
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Ygapop 10.0 , Ygapext 0.5  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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7	786	23.6	770	4	CB423984	CB423984 605838 MA
8	756	22.7	602	5	CD708943	CD708943 EST25470
9	707	21.3	825	12	CC496590	CC496590 CH240_332
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19	257	7.7	844	12	CC515253	CC515253 CH240_360
20	256.5	7.7	1512	6	BC020454	BC020454 Mus muscu
21	244.5	7.4	619	4	BX736370	BX736370 BX736370
22	240.5	7.2	3055	6	AY310138	AY310138 Rattus no
23	240	7.2	949	3	BU913664	BU913664 AGENCOURT
24	218	6.6	794	14	CT440157	CT440157 Sus scrof
25	205.5	6.2	5264	6	BC071555	BC071555 Homo sapi
26	199.5	6.0	1822	6	CNSOPOM	CR650198 Tetradon
27	199	6.0	672	11	AZ418811	AZ418811 IM0195J03
28	195	5.9	4460	6	CR858901	CR858901 Pongo pyg
29	192	5.8	695	14	CT346894	CT346894 Sus scrof
30	191.5	5.8	628	4	CB427282	CB427282 602850 MA
31	189	5.7	704	14	CR102197	CR102197 Forward 8
32	187.5	5.6	887	5	CF780723	CF780723 AGENCOURT
33	187	5.6	626	4	CA893723	CA893723 B0181A01-
34	181.5	5.5	2804	6	AK089305	AK089305 Mus muscu
35	181.5	5.5	3948	6	AK144318	AK144318 Mus muscu
36	178.5	5.4	699	4	CB168262	CB168262 HSF603268
37	177.5	5.3	1455	9	DN685150	DN685150 CGX40-B05
38	177	5.3	1402	6	CNSOPSV8	CR686776 Tetradon
39	175.5	5.3	2535	14	AY412154	AY412154 Mus muscu
40	174.5	5.2	2815	6	AK155864	AK155864 Mus muscu
41	173	5.2	4145	6	AK155524	AK155524 Mus muscu
42	169	5.1	695	4	BX849563	BX849563 BX849563
43	168.5	5.1	584	9	DB238786	DB238786 DB238786
44	168.5	5.1	909	14	AY416683	AY416683 Pan trogl
45	167.5	5.0	635	2	BM489310	BM489310 pgm2n.pk0

## ALIGNMENTS

RESULT 1  
BQ228535  
LOCUS  
DEFINITION  
AGENCOURT\_7594648 NIH\_MGC\_72 Homo sapiens cdna clone IMAGE:6061504  
5', mRNA sequence.  
ACCESSION  
BQ228535  
VERSION  
BQ228535.1 GI:20409935  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
REFERENCE  
NIH-MGC http://mgc.nci.nih.gov/  
TITLE  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL  
Unpublished (1999)  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cga@nci.nih.gov  
Tissue Procurement: ATCC/DC/DT/DTP  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: L1AM1331 row: h column: 17  
High quality sequence stop: 554.

FEATURES  
 source  
 Location/Qualifiers  
 1. 916  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6061504"  
 /issue\_type="melanotic melanoma"  
 /lab\_host="DH10B (phage-resilient)"  
 /clone\_lib="Nih MGc 72"  
 /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."

## ORIGIN

## Alignment Scores:

Pred. No.: 2,85e-103 Length: 916  
 Score: 1009.00 Matches: 223  
 Percent Similarity: 66.0% Conservative: 8  
 Best Local Similarity: 63.7% Mismatches: 27  
 Query Match: 30.3% Indels: 93  
 DB: 3 Gaps: 6

US-10-667-289-2 (1-629) x BQ228535 (1-916)

QY 265 TTPAan-VallysglupheapThrAanpThrTyValgIngsInsergiupheTyLe 284  
 Db 66 TGAACCTGTTAAAGATTGACACCAATTATACATATGTCACACAGTCAGAAATCTT 125  
 QY 284 uGluProbenlleystryValpHeGlnValaGyGgIngluThrglylyAaGgYTr 304  
 Db 126 GGAACCAACATTAAGTACGTAATTCAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 185  
 QY 304 pGluProTpserserProPhepHehilyeThrProgluThrValProgluValTrse 324  
 Db 186 GCAACCTTGAGTTCACTGTTTTCATTAACCACTGAA----- 225  
 QY 324 rlyAlaPheGlnHisapThrTPAanSerglyLeuThrValAlaSerIleSerrhG 344  
 Db 225 ----- 225  
 QY 344 yHleuThrsersapHnAgtgIyaepIleglyLeuLeuLeuGlyMetIleValPheAl 364  
 Db 225 ----- 225  
 QY 364 aValMetIleuserIleuserLeuIleglyIlePheanAgserserPheargThrglyI 384  
 Db 226 -----ACAGATT 233  
 QY 384 elyAaGArgIleleuLeuLeuIleProlySTrPLeuTyGluAplleProAanMetly 404  
 Db 234 -AAAGAAGAGATCTTATGTTAATACCAAGTGGCTTATGATGATATTCCTAATATGA 292  
 QY 404 sAanSerAanVallylyshMetLeuGlnGluAanSerglyLeuMetAanAanSers 424  
 Db 293 AAACAGCAATGTTGTGAAAAGCTACAGAAAAGTGAACCTTATGAATATAATTCAG 352  
 QY 424 rGluGlnValleuTyrrAlaAapPrometIleThrgluIlelyGgIngluIlePheIleProgl 444  
 Db 353 TGAACAGTCTTATATGTTATCCCAATGATTAACAGATTAAGAAATCTTCAATCCAGA 412  
 QY 444 uHlelyPProThraPTrlylylysgluAanThrglyProleuGlnuThrAaPTrlyPr 464  
 Db 413 ACACAGCCTACACACTACAGAGAGAAATACAGAGAGAGAGAGAGAGAGAGAGAGAG 472  
 QY 464 oGlaAanSerleuPheapAanThrThrVallylyrIleProapleuAanThrglyTy 484  
 Db 473 GCAAAACCTCGCTATTCACATATACATACAGTTGTATATTCCTATCTCAACACTGATA 532  
 QY 484 rlyAProgluIleSerAanPheleuProgluGlySerHileuserAanAanSerglyI 504  
 Db 533 TAAACCCCAATTCATTAATTTTCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 592

QY 504 eThrSerleuThrleuAapProPro-ValapSerleuAapSerglyAanAanProAarg- 523  
 Db 593 TACTTCTTAACACTTAACACACAGGTATCTTACATCAGCAATATATCCAGAG 652  
 QY 524 LeuGlnlyHisPro-AanPheAlaPhe-----SerrValSers 536  
 Db 653 TTAACAAAGCATCTTAATTTGTTTCTGTTCCAAAGGGGAAATTTCCCTAACCA 712  
 QY 536 rValAanSerleuSerrAanThrIlePheLeuGlyGluLeuSerleuIleleuAanGln 556  
 Db 713 ACCCAAT-----ATTCTTTGAGAAATTAAGCTCTTATTAATCAG 757  
 QY 556 yGlu-----CysSerSerProapIleGlnAanSerrValgIngluGluThrMetle 574  
 Db 758 GGAAGATGACATTCTTCCTGAACTTAACCAACTCCCTTGAAGAGAGAAACCCCT 817  
 QY 574 uLeu-----GluAanSersPro-----SerrGluThrI 584  
 Db 818 GACTTTTGAGAAAGATTTCCCGGGGAAACTATTTCACAAAAAACCCGGGCT 877  
 QY 584 eProgluGlnThrleuAapPro 591  
 Db 878 TCCTGAGAGAAATTTGGCCCC 899

RESULT 2  
 BP282008 583 bp mRNA linear EST 16-SEP-2004  
 LOCUS BP282008 Sugano cDNA library, bone marrow K562 Homo sapiens cDNA  
 DEFINITION clone KMR03033, mRNA sequence.  
 ACCESSION BP282008  
 VERSION BP282008.1 GI:52195740  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo.

REFERENCE  
 AUTHORS Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,  
 Mizushima-Sugano, J., Nakai, K. and Sugano, S.  
 TITLE Sequence comparison of human and mouse genes reveals a homologous  
 block structure in the promoter regions  
 JOURNAL Genome Res. 14 (9), 1711-1718 (2004)  
 PUBMED 15342556  
 COMMENT Contact: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Tel: 81-3-5449-5343  
 Fax: 81-3-5449-5416  
 Email: yusuzuki@igc.jp.

FEATURES  
 source  
 Location/Qualifiers  
 1. 583  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="KMR03033"  
 /issue\_type="bone marrow"  
 /cell\_line="K562"  
 /note="Sugano cDNA library, bone marrow K562"  
 /note="chronic myelogenous leukemia"

## ORIGIN

## Alignment Scores:

Pred. No.: 1.44e-88 Length: 583  
 Score: 877.00 Matches: 168  
 Percent Similarity: 99.4% Conservative: 0  
 Best Local Similarity: 99.4% Mismatches: 0  
 Query Match: 26.4% Indels: 1  
 DB: 3 Gaps: 0

US-10-667-289-2 (1-629) x BP282008 (1-583)



QY 265 TTPAsn-VallyeGluPheAspThrAsnPherThyValGInGlnSerGluPheTyLe 284  
 Db 78 TGGAACTGTTAAAGAAATTGACCAATTTTACATATGTGCAACAGTCAGAAATTCATCTT 137  
 QY 284 UGIUProAsnIleuTyValPheGlnValArgCyGlnGlnIuThrgIyLyAspGlyrTr 304  
 Db 138 GGAGCCAAACATTAAGTACGATTTTCAAGTGAATGTCAGAAACAGGCAAAAGGTACTG 197  
 QY 304 PGInProTTrSerSerProPhePheHISlySThrProGluThrValProGlnValThrSe 324  
 Db 198 GCGACCTTGAGTTCCACCGTTTTTTCATTAACACCTGAAACAGTTCCTCCAGGTCAATC 257  
 QY 324 rLySaIaPheGlnHISAspThrTPAsnSerGlyLeuThrValAlaSerIleSerThrgI 344  
 Db 258 AAAAGCATTCACATGACATGCAATTCGGCTCAAGTTCCTCCATCTTACACGG 317  
 QY 344 YHISleuThrSerAspAsnArgIyAspIleGlyLeuLeuLeuGlyMetIleValPheAl 364  
 Db 318 GCACCTTACTTCTGACAAACAGAGACATTCGATTTTATGGGAATGATCGCTTTCG 377  
 QY 364 aValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPheArgThrgIyI 384  
 Db 378 TGTATGTTGTCAATTCCTTTCTTGATGGGATATTTAAACAGATCATTCGAACTGGGAT 437  
 QY 384 eLyAspArgIleLeuLeuLeuIleProLySTrPLeuTyGluAspIleProAsnMetLy 404  
 Db 438 TAAAGAGAGATCTTATTTGTTAAACCAAGTGGCTTTATGAGATATTCCTAATATGAA 497  
 QY 404 SAASerAsnValIyISleuLeuGlnGlnIuAsnSerGlyLeuMetAsnAsnAsnSerSe 424  
 Db 498 AAACAGCAATGTTGTGAAATGCTACAGAAATAGCAATCTTATGATATATATTCAG 557  
 QY 424 rGluGlnValLeuTyValAspPro 432  
 Db 558 TGAGCAGCTCTATATGTATGATCC 582

RESULT 3  
 BF210400 754 bp mRNA linear EST 06-NOV-2000  
 LOCUS 60187448.F1 NIH\_MGC\_54 Homo sapiens cDNA clone IMAGE:4101164 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BF210400  
 VERSION BF210400.1 GI:11103966  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo.  
 1 (bases 1 to 754)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: rgs@ds-rs.fda.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: CLONTECH Laboratories, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: LNC972 row: 9 column: 21  
 High quality sequence stop: 650.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4101164"  
 /issue\_type="from chronic myelogenous leukemia"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_id="NIH\_MGC\_54"

## FEATURES

source  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4101164"  
 /issue\_type="from chronic myelogenous leukemia"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_id="NIH\_MGC\_54"

/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);  
 Site 1: Sfil (ggcgctcgccg); Site 2: Sfil  
 (ggcctatggcc); Double-stranded cDNA was prepared from  
 cell line RNA. 5' and 3' adaptors were used in the  
 following: 5' adaptor sequence: 5'-CACGCCATTAATGCG-3' and  
 3' adaptor sequence:  
 5'-ATTCAGAGCCGAGCGCCGACATG-dt(30)BN-3' (where B = A,  
 C, or G and N = A, C, G, or T). Average insert size  
 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained  
 inserts by PCR. This library was enriched for full-length  
 clones and was constructed by Clontech Laboratories (Palo  
 Alto, CA)."

## ORIGIN

## Alignment Scores:

Pred. No.:	414e-86	Length:	754
Score:	857.00	Matches:	189
Percent Similarity:	91.9%	Conservative:	14
Best Local Similarity:	85.5%	Mismatches:	12
Query Match:	25.8%	Indels:	11
DB:	7	Gaps:	4

US-10-667-289-2 (1-629) x BF210400 (1-754)

QY 265 TTPAsn-VallyeGluPheAspThrAsnPherThyValGInGlnSerGluPheTyLe 284  
 Db 78 TGGAACTGTTAAAGAAATTGACCAATTTTACATATGTGCAACAGTCAGAAATTCATCTT 137  
 QY 284 UGIUProAsnIleuTyValPheGlnValArgCyGlnGlnIuThrgIyLyAspGlyrTr 304  
 Db 138 GGAGCCAAACATTAAGTACGATTTTCAAGTGAATGTCAGAAACAGGCAAAAGGTACTG 197  
 QY 304 PGInProTTrSerSerProPhePheHISlySThrProGluThrValProGlnValThrSe 324  
 Db 198 GCGACCTTGAGTTCCACCGTTTTTTCATTAACACCTGAAACAGTTCCTCCAGGTCAATC 257  
 QY 324 rLySaIaPheGlnHISAspThrTPAsnSerGlyLeuThrValAlaSerIleSerThrgI 344  
 Db 258 AAAAGCATTCACATGACATGCAATTCGGCTCAAGTTCCTCCATCTTACACGG 317  
 QY 344 YHISleuThrSerAspAsnArgIyAspIleGlyLeuLeuLeuGlyMetIleValPheAl 364  
 Db 318 GCACCTTACTTCTGACAAACAGAGACATTCGATTTTATGGGAATGATCGCTTTCG 377  
 QY 364 aValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPheArgThrgIyI 384  
 Db 378 TGTATGTTGTCAATTCCTTTCTTGATGGGATATTTAAACAGATCATTCGAAAT-GGGAT 436  
 QY 384 eLyAspArgIleLeuLeuLeuIleProLySTrPLeuTyGluAspIleProAsnMetLy 404  
 Db 437 TAAAGAGAGATCTTATTTGTTAAACCAAGTGGTT-TATGAGATATTCCTAATATGAA 495  
 QY 404 SAASerAsnValIyISleuLeuGlnGlnIuAsnSerGlyLeuMetAsnAsnAsnSerSe 424  
 Db 496 AAACAGCAATGTTGTGAAATGCTACAGAAATAGCAATCTTATGATATATATTCAG 555  
 QY 424 rGluGlnValLeuTyValAspProMetIleThrgIuIleGlnIuIlePheIleProG 444  
 Db 556 TGAGCAGCTCTATATGTATTCCTTATGATGGGATATTTAAACAGATCATTCGAAAT-CA 611  
 QY 444 uHISlyPProThAspTyIyISlyGluAsnThrgIyProLeuGlnIuThrAspTyPr 464  
 Db 612 GAACAAAGCTACAGATCTACAGAAAGG-AATACAGACCTCGGAGC---AGAGAAAT-CC 666  
 QY 464 OGInAsnSerLeuPheAspAsnThrValIyIlePheAspLeuAsnThrgIy 484  
 Db 667 GGAAGAT---TGGTATTCGAATACATCAAGTGTTCG-----ATTCAACTGGTT 717  
 QY 484 r 484  
 Db 718 T 718

RESULT 4

BF209716 820 bp mRNA linear EST 06-NOV-2000  
 LOCUS 601874259F1 NIH\_MGC\_54 Homo sapiens cDNA clone IMAGE:4098831 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BF209716  
 VERSION BF209716.1 GI:11103302  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 820)  
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cga@ds-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: CLONTECH Laboratories, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: LNCM966 row: f column: 16  
 High quality sequence stop: 608.  
 Location/Qualifiers  
 1..820  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4098831"  
 /tissue\_type="from chronic myelogenous leukemia"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NIH\_MGC\_54"  
 /note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);  
 Site 1: SfiI (ggcgccctcgcc); Site 2: SfiI  
 (ggcctatcgcc); Double-stranded cDNA was prepared from  
 cell line RNA. 5' and 3' adaptors were used in cloning as  
 follows: 5' adaptor sequence: 5'-CACGGCCATTATGCCC-3' and  
 3' adaptor sequence:  
 5'-ATTGAGGCCGAGCGCCGACATG-dt(30)BN-3' (where B = A,  
 C, or G and N = A, C, G, or T). Average insert size  
 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained  
 inserts by PCR. This library was enriched for full-length  
 clones and was constructed by Clontech Laboratories (Palo  
 Alto, CA)."  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 2,56e-83 Length: 820  
 Score: 833.00 Matches: 182  
 Percent Similarity: 89.8% Conservative: 3  
 Best Local Similarity: 88.3% Mismatches: 14  
 Query Match: 25.0% Indels: 8  
 DB: 7 Gaps: 0  
 US-10-667-289-2 (1-629) x BF209716 (1-820)  
 Oy 431 AASPProctetierhngluileysguilepheileproglunilalyprothaspyr 450  
 Db 1 GATCCCATGATTACGAGATAAAGAAATCTTCATCCGAAACCAAGCTCAGACTAC 60  
 Oy 451 LysAlsguuanthnglyProleugluThrtarapsyrrProglinaerSetleupheasp 470  
 Db 61 AAGAGAGGAGATACAGATCCCTGGAGCAAGAGACTACCGCAAAACTCCCTATTGGAC 120  
 Oy 471 AantThrtValaValTYrileProaspheuanthnglyTYrlyProglilSeasn 490  
 Db 121 AATCTACAGTTGTATATATCTCGATCTCAACACTGATTAACCCCAATTTCAAT 180  
 Oy 491 PheleuproguglySerHisleuseraanaangluilethrsertleuthrleuys 510

Db 181 TTTCTGCTTAGGAGGAGCCATCTCAGCAATTAATGAATTAATCTTCTTAACATT-AAA 239  
 Oy 511 ProProValaApsSerleuaApsSerGlyAanaApsProAgtleugluYrHisProApsPhe 530  
 Db 240 CCACCACTTAATCTCTTAAGCTCAGGAAATATATCCCGATTACAAAAGCATCTTAATTG 299  
 Oy 531 AlApsSerValSerSerValaApsSerleuSerApsAnthrillepheleuglyguLeuSer 550  
 Db 300 GCTTTCTGTTTCAAAAGTGTGAATTCCTAAGCAACACATATTTCTGTGAGAAATTAGC 359  
 Oy 551 LeuulleuAangluYguYrSerSerProaspille-GluApsSerValGluGlu 570  
 Db 360 CTATATTAATCAAGAGATACAGATCTCCGACATTAACAAACTACGTAGAGAGGA 419  
 Oy 570 UThrtThMetleu-LeuGluAanaApsSerProserguThrtilleProgluGluThrleu 590  
 Db 420 AACCACTATGCTTTGTGAAATATGATTCACCCAGTGAATTCAGAACCAAGACTGC 479  
 Oy 590 eupProApsGuIuphe-ValSerCys-LeuGlyileValaanglu-GluLeuProSerilleA 609  
 Db 480 TTCTGATGATGATTTGGTCTCTGTTTGGGATTCGTGAATGAAGAGAGTGGCATCTATTA 539  
 Oy 609 enthrTYrPheProglu-Aanlle-LeuGluSerHisApsAanArglApsSerleuGlu 628  
 Db 540 ATATTATTTTCCACAAATAATTTGTGAAAGCCACTTCATATGATTTCACTCTGGG 599  
 Oy 628 ulys 629  
 Db 600 CAA 603  
 RESULT 5  
 BF28439 917 bp mRNA linear EST 14-NOV-2000  
 LOCUS 601904735F1 NIH\_MGC\_54 Homo sapiens cDNA clone IMAGE:4132593 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BF28439  
 VERSION BF28439.1 GI:1152359  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 917)  
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cga@ds-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: CLONTECH Laboratories, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: LNCM1032 row: e column: 10  
 High quality sequence stop: 575.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4132593"  
 /tissue\_type="from chronic myelogenous leukemia"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NIH\_MGC\_54"  
 /note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);  
 Site 1: SfiI (ggcgccctcgcc); Site 2: SfiI  
 (ggcctatcgcc); Double-stranded cDNA was prepared in cloning as  
 follows: 5' adaptor sequence: 5'-CACGGCCATTATGCCC-3' and

3' adaptor sequence:  
 5'-ATTCTAGAGCGGAGCGCGCATG-dr(30)BN-3' (where B = A,  
 C, or G and N = A, C, G, or T). Average insert size  
 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained  
 inserts by PCR. This library was enriched for full-length  
 clones and was constructed by Clontech Laboratories (Palo  
 Alto, CA)."

## ORIGIN

## Alignment Scores:

Pred. No.:	2.86e-82	Length:	917
Score:	824.50	Matches:	185
Percent Similarity:	88.8%	Conservative:	6
Best Local Similarity:	86.0%	Mismatches:	18
Query Match:	24.8%	Indels:	10
DB:	7	Gaps:	1

US-10-667-289-2 (1-629) x BF238439 (1-917)

265 TTPAsn-VallysGluPheApThrAnPheThrTyValGlnGlnSerGluPheTyLe 284  
 78 TGGAACTGTAAAGAAATTTGACCAATTTTACATATGTGACACAGTCAGAAATCTTACTT 137  
 284 UGUProAsnIleTySerTyValPheGlnValArgCysGlnGlnThrGlyValArgTyTyT 304  
 138 GGAGCCAAACATTAAGTACGATTTCAAGTACGATGTCAGAAACAGGCAAAAGTACTG 197  
 304 PGINProTTPSerSerProPhePheHisTySerThProGlnThrValProGlnValThrSe 324  
 198 GCAGCCTTGAAGTTCACCGTTCATTTTCAAAAACATGAAACATTTCCCGGTCACATC 257  
 324 TlyValAlPheGlnHisApThrThTPAsnSer-GlyLeuThrValAlaserIleSerThrg 344  
 258 AAAAGCATTCACACATGACACATGGAATTCGGGGCTTACAGCTTCTTCATCTCTACG 317  
 344 TlyHisLeuThrSerAspAsnArgGlyAspIleGlyLeuLeuLeuGlyMetIleValPhe 364  
 318 GGCACTTACTTCTGACACAGAGAGACATTTGACCTTTTATGGAATGATCGCTTTG 377  
 364 lAlValMetLeuSerIleLeuSerIleuIleGlyIlePheAsnArgSerPheArgThrgIy 384  
 378 CTGTTATGTGTCAATCTTCTTCTTGAAGGAGATTTTAAACAGATTCATTCGAACCTGGGA 437  
 384 lelysArgArgIleLeuLeuLeuIleProIySTPLeuTyGluAspIleProAsnMet 404  
 438 TTACAGAGAGATCTTATG-TTAAATACCAAGTGGCT-TATGAAAGATTTCTTAATATGA 495  
 404 YsaAsnSerAsnValIleTyMetLeuGlnGlnAsnSerGluLeuMetAsnAsnAsnSers 424  
 496 AAAACACCAATGTTGTGAAAATGCTACAGAAAATAGGAATCTTATGAATATATATCCA 555  
 424 er-GluGlnValLeuTyValAspProMetIleThrgIuile-LysGluIlePheIlePr 443  
 556 GTTACAGAGAGCTATATGTTGATCNCAATGATTAACGAGATACACAGAAATTCATCC 615  
 443 OGluHisTySerProThrAspTyTyValGlyGluAsnThrClYProLeuGluThrArgAspTy 463  
 616 AGAATAA-AAAGCTACAGCTACAGAAAGGAGCTA-CAGGACCTGGGAAAGAGAGA----- 668  
 463 rProGlnAsnSerLeuPheAspAsnThrThValVal 475  
 669 -TAACCGAAATCGCTATTCGAAAATATCACTACGCTGTA 704

RESULT 6  
 BF238869 823 bp mRNA linear EST 14-NOV-2000  
 LOCUS 601904492P1 NIH\_MGC\_54 Homo sapiens cDNA clone IMAGE:4132295 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BF238869  
 VERSION BF238869.1 GI:11152790  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS NIH-MGC  
 TITLE NIH-MGC  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: CLONTECH Laboratories, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: LNCM1031 row: h column: 24  
 High quality sequence stop: 584.

## FEATURES

## source

1. .823  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4132295"  
 /issue\_type="from chronic myelogenous leukemia"  
 /lab\_host="DH10B (T1 phase-resistant)"  
 /clone\_1lb="NIH MGC 54"  
 /note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);  
 Site 1: SfiI (ggcgctcgcc); Site 2: SfiI  
 (ggccatcagcc); Double-stranded cDNA was prepared from  
 cell line RNA. 5' and 3' adaptors were used in cloning as  
 follows: 5' adaptor sequence: 5'-CACGGCCATTATGCGC-3' and  
 3' adaptor sequence:  
 5'-ATTCTAGAGCGGAGCGCGCATG-dr(30)BN-3' (where B = A,  
 C, or G and N = A, C, G, or T). Average insert size  
 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained  
 inserts by PCR. This library was enriched for full-length  
 clones and was constructed by Clontech Laboratories (Palo  
 Alto, CA)."

## ORIGIN

## Alignment Scores:

Pred. No.:	7.09e-79	Length:	823
Score:	794.00 <td>Matches:</td> <td>190</td>	Matches:	190
Percent Similarity:	69.1%	Conservative:	16
Best Local Similarity:	63.8%	Mismatches:	25
Query Match:	23.9%	Indels:	72
DB:	7	Gaps:	4

US-10-667-289-2 (1-629) x BF238869 (1-823)

265 TTPAsn-VallysGluPheApThrAnPheThrTyValGlnGlnSerGluPheTyLe 284  
 75 TGGAACTGTAAAGAAATTTTACCAATTTTACATATGTGACACAGTCAGAAATCTTACTT 134  
 284 UGUProAsnIleTySerTyVal-PheGlnValArgCysGlnGlnThrGlyValArgTyTyT 304  
 135 GGAGCCAAACATTAAGTACGATTTCAAGTACGATGTCAGAAACAGGCAAAAGTACT 194  
 304 PGINProTTPSerSerProPhePheHisTySerThProGlnThrValProGlnValThrS 324  
 195 GCAGCCTTGAAGTTCACCGTTCATTTTCAAAAACATGAAACAGTCCCCAGGTCAAT 254  
 324 TlyValAlPheGlnHisApThrThTPAsnSerGlyLeuThrValAlaserIleSerThrg 344  
 255 CAAAAGATTCACACATGACACATGGAATTCGGGCTTACAGATTCCTTCAATCTTACG 314  
 344 TlyHisLeuThrSerAspAsnArgGlyAspIleGlyLeuLeu-LeuGlyMetIleValPhe 363  
 315 GGCACTTACTTCTGACACAGAGAGACATTTTATGGAATGATCGCTTTT 374  
 364 lAlValMetLeuSerIleLeuSerIleuIleGlyIlePheAsnArgSerPheArgThrgIy 383

Db 375 GCTGTATGTCGCAATTCCTTCTTGATGGGATATTAAACAGATCATTCGCACTGGG 434  
Qy 384 TLeysArgArgIleLeuLeuLeuIleProlyStryLeuTyrgIuAapIleProAsnMet 403  
Db 435 ATTTAAAGAGAGATCTTATTCTTATTACCAAGTGTT-TATGAAGATATTCTTAATATG 493  
Qy 404 LysAsnSerAsnValIvalMetLeuGlnIuAn-SerGluLeuMetAsnAsnSe 423  
Db 494 AAAAAGACGAT-GTTGTGAAAATGCTACAGAAAATAGGGAGACTTAATTAATTC 552  
Qy 423 rSerGluGlnValLeuTyrgIuAapPrometIleThrGluIleLeuGluIlePheIlePr 443  
Db 553 CAGTGAAGAGGT-CTAATGTGTGATCCCATGATTAACGAGAT-AAAGAAATCTTCAT-CC 609  
Qy 443 OGLuHISlySerProThrAsp-----TyrgIySgluAenThrGlyPr 457  
Db 610 AGAACACAGACGCTACAGTACAGAGGGATACGGCCCTGGGGACACAGAAATACGGG-- 667  
Qy 457 OLeuGluThrArgAspTyrgIuAenSerLeuPheAsnThrThrValIleTyrl 477  
Db 668 -----AAATCGTATCGCAACACAGCGGTTTTCTGTCAATGGTT----- 709  
Qy 477 eProAspLeuAsnThrGlyTyrgIySProGlnIleSerAsnPheLeuProGluGlySerH 497  
Db 709 ----- 709  
Qy 497 sLeuSerAsnAsnGlnIleThrSerLeuThrLeuTyrgIySProValAspSerLeuAs 517  
Db 709 ----- 709  
Qy 517 pSerGlyAsnAsnProArgLeuGlnIySHisProAsnPheAlaPheSerValSerSerVa 537  
Db 710 -----AACCAATTATTGCGGGGCGCGGAAATGATAT----- 745  
Qy 537 lAsnSerLeuSerAsnThrIlePheLeuGlyGluLeuSerLeuIle 552  
Db 746 -----CTTACTACACAGCGTCTTCTCGAAACCGTGAATCTTGTT 784

RESULT 7  
CB429984/c 720 bp mRNA linear EST 25-MAR-2003  
LOCUS CB429984 605838 MRC BOV Bos taurus cDNA 3', mRNA sequence.  
ACCESSION CB429984  
VERSION CB429984.1 GI:29205578  
KEYWORDS EST.  
SOURCE Bos taurus (cattle)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Bovidae; Bovinae; Bos.  
1 (bases 1 to 720)  
Smith,T.P.L., Roberts,A.J., Scherinkamp,S.B., Chitko-Mckown,C.G.,  
Wray,J.B. and Keele,J.W.  
A second set of bovine ESTs from pooled-tissue normalized libraries  
unpublished (2003)  
Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4356  
Fax: 402 762 4350  
Email: smtthe@mail.marc.usda.gov  
Single pass sequencing. Bases called with phred v0.020425.c and  
trimmed with the aid of the trim\_alt option. Vector identified with  
cross\_match v0.990329.  
Plate: F0Y8023 row: G column: 9  
Seq primer: TAGAAGGACAGTCGAG.  
Location/Qualifiers  
1..720  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/tissue\_type="pooled"  
/lab\_host="DH10B"

## FEATURES

SOURCE

/clone\_lib="MARC 6BOV"  
/note="Vector: pCDNA3.1; Site\_1: EcoRI; Site\_2: NotI;  
library made with RNA pooled from multiple tissues  
including liver, lung, hypothalamus, pituitary, and  
placenta/endometrium."

## ORIGIN

Alignment Scores:  
Pred. No.: 4,64e-78 Length: 720  
Score: 786.00 Matches: 154  
Percent Similarity: 64.6% Conservative: 12  
Best Local Similarity: 59.9% Mismatches: 13  
Query Match: 23.6% Indels: 78  
DB: 4 Gaps: 1

US-10-667-289-2 (1-629) x CB429984 (1-720)

Qy 11 ValIleAlaLeuTyrgIleLeuPheSerTrpCyHisGlyGlyIleThrAsnIleAsnCyS 30  
Db 716 GTATATACCTCTCAATATTCCTCAGTGGTGCATGAGAGGATTAACAAATATAACTGC 657  
Qy 31 SerGlyHisIleTrpValGluProAlaThrIlePheIySmetGlyMetAsnIleSerIle 50  
Db 656 TCTGGACACATCTGGGGTGAACCTGCACAAATTTTAAAGATGAT----- 612  
Qy 51 TyrgIySgluAlaAlaIleIySAsnCySgluProArgIySleuHisPheTyrgIySAsnGly 70  
Db 612 ----- 612  
Qy 71 ILeuSgluArgPheGlnIleThrArgIleAsnIySThrAlaArgLeuTrpTyrgIyS 90  
Db 612 ----- 612  
Qy 91 AsnPheLeuGluProHisAlaSerMetTyrgIySThrAlaGluCySProIySHISpHeGln 110  
Db 612 ----- 612  
Qy 111 GluThrLeuIleCySgluYsAspIleSerSerGlyTyrgIySProProAspIleProAspGlu 130  
Db 611 -----CCACGAGATGTACTTGACAAA 591  
Qy 131 ValThrCySValIleTyrgIySLeuTyrgIySAsnMetThrCySThrTrpAsnAla\*\*Lys 150  
Db 590 GTAGCCGTGTATATTAATTAATTAATTTCTGGCAACATGACTTGACCTGGAACCATGGAGG 531  
Qy 151 LeuThrTyrgIleAspThrIySArgValIleHisValIySLeuSerLeuGluThrGluGlu 170  
Db 530 CCACCTTACATGACACAAAGATATGTGTACCTGAAGAGTTTGAAGACAGAAAGAG 471  
Qy 171 GlnGlnTyrgIleuThrSerSerTyrgIleAsnIleSerThrAspSerLeuGlnGlyIyS 190  
Db 470 CAAGAAATATCTCACTTCACAGTTACATTAATCTCCACTGATTCATTCGAAAAGGGCAG 411  
Qy 191 LysTyrgIleuValTrpValGlnAlaAlaAsnAlaLeuGlyMetGluGlySerIySgluLeu 210  
Db 410 AAGTATTTGGTTGGGTCGCAAGCTCAAAAGTTCTGGGCATGGAGAGTGAACCAACTA 351  
Qy 211 GlnIleHisLeuAspAspIleValIleProSerAlaAlaValIleSerArgAlaGluThr 230  
Db 350 CAATTCATCTGACGACATATAGATATCTTCTGCATCCATTAATTCAGAGGCTGAGAGAT 291  
Qy 231 ILeuAlaLeuThrValProIySThrIleIleTyrgIySAspSerGlnThrIleGluIyS 250  
Db 290 ATAAATACCTACAGTGCACAGACGTGATACACTGAGATGTCACATCATCATTAAGAAAA 231  
Qy 251 ValSerCySgluMetArgIySValAlaThrThrAsnGlnThrTrpAsnVal 267  
Db 230 GTTTCCTGTGAATGAGATCAAAAGATACAAACCAAACTTGAGACGTA 180

## RESULT 8

LOCUS

CD708943 602 bp mRNA linear EST 25-JUN-2003  
DEFINITION EST25470 human nasopharynx Homo sapiens cDNA, mRNA sequence.

ACCESSION CD708943  
VERSION CD708943.1 GI:32239573  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
REFERENCE 1 (bases 1 to 602)  
AUTHORS Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and  
Zeng, Y.-X.  
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx  
JOURNAL Unpublished (2003)  
COMMENT Contact: Yixun Zeng  
Cancer Center  
Sun Yat-sen University  
651 Dongfeng Road East, Guangzhou 51060, China  
Tel: 86-1380-9770-743  
Fax: 86-20-8775-4506  
Email: yxzeng@gzsums.edu.cn.  
FEATURES  
source  
1..602  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/issue\_type="normal nasopharynx"  
/clone\_lib="human nasopharynx"  
/note="ESTs generated from a normal nasopharynx cDNA  
library from southern Chinese"

ORIGIN  
Alignment Scores:  
Pred. No.: 8,99e-75 Length: 602  
Score: 756.00 Matches: 135  
Percent Similarity: 99.3% Conservative: 0  
Best Local Similarity: 99.3% Mismatches: 1  
Query Match: 22.7% Indels: 0  
Gaps: 0  
DB: 5

US-10-667-289-2 (1-629) x CD708943 (1-602)

QY 1 MetAan\*\*ValThrIleGlnTrpAspAlaValIleAlaLeuTyrIleLeuPheSerTrp 20  
Db 194 ATGAATCATGTCTACTATTCATATGAGATCGCATATATACCCCTTTCATACCTTCAGCTGG 253

QY 21 CyshIsgIyGlyIleThrAenIleAenCySerGlyHisIleTrpValIleGluProAlaThr 40  
Db 254 TGTCAATGAGGAATTAACAATATTAATGCTGCGCACATCTGGTAGAACACAGCACA 313

QY 41 IlePheIleMetGlyMetAenIleSerIleTyrCysGlnIleAlaIleIleAenCysGln 60  
Db 314 ATTTTAAAGAGGTATGAATATCTATATATGCGCAAGACGAATTAAGAACTGCGCAA 373

QY 61 ProArgIleLeuHisPheTyrIleAenGlyIleIleGluIleArgPheGlnIleThrArgIle 80  
Db 374 CCAAGGAACCTCTCTTTTAAATAATGCGATCAAAAGAACTTCAATACACAGAAATT 433

QY 81 AsnIleThrThrAlaArgLeuTyrIleAenPheLeuGluProHisAlaSerMetTyr 100  
Db 434 AATTAACAACAGCTCGCTTGTATATAAACTTTCGGAACACATGCTTCTATGTAC 493

QY 101 CysThrIleAlaGluCysProIleHisPheGlnIleThrLeuIleCysGlyIleAenIleSer 120  
Db 494 TGCATGCTGAATGCTCCAAACATTTTCAAGAGACACTGATATGTGAAAAAGACATTTCT 553

QY 121 SerGlyTyrProProAspIleProAspGluValThrCysValIleTyr 136  
Db 554 TCTGGATATCCGCCAGATATTCCTGATGAAGTAACCTGTGCAATTAT 601

RESULT 9  
CC496590 825 bp DNA linear GSS 17-JUN-2003  
LOCUS CC496590  
DEFINITION CH240\_332J15.TARBAC13P2 CHORI-240 Bos taurus genomic clone

ACCESSION CH240\_332J15, genomic survey sequence.  
VERSION CC496590  
KEYWORDS CC496590.1 GI:31811154  
SOURCE GSS.  
ORGANISM Bos taurus (cattle)  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Pecora; Bovidae; Bovinae; Bos.  
REFERENCE 1 (bases 1 to 825)  
AUTHORS Holt, R., Stott, J., Yang, G., Barber, S., Smailus, D., Prabh, A.-L.,  
Teal, M., Cloutier, A., Lee, D., Gilm, N., Olson, T., Mayo, M.,  
Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A.,  
Mathewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S.,  
Schein, J., Marra, M., de Jong, P., McWilliam, S., Barris, W.,  
Dalrymple, B.P. and Tellam, R.  
TITLE Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398  
JOURNAL Unpublished (2003)  
COMMENT Other GSSs: CH240\_332J15.T7  
Contact: Rob Holt  
Sequencing  
The British Columbia Cancer Agency Genome Science Centre  
600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4B6  
Tel: 604-877-6085  
Fax: 604-877-6276  
Email: holt@bccgsc.ca  
Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm). For BAC library  
availability, please contact Pieter de Jong (pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering/information.htm). This work  
was undertaken as part of the International Bovine BAC Mapping  
Consortium (IBMC) by CSIRO Livestock Industries, Australia and the  
British Columbia Genome Sciences Centre, Canada.  
Plate: 332 row: J Column: 15  
Seq primer: SP6  
Class: BAC ends.  
FEATURES  
source  
1..825  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="b:reel: Hereford"  
/db\_xref="taxon:9913"  
/clone\_lib="CH240\_332J15"  
/sex="male"  
/cell\_type="Blood"  
/clone\_lib="CHORI-240"  
/note="vector: PTARBAC1.3; Site 1: MboI, site 2: MboI;  
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

ORIGIN  
Alignment Scores:  
Pred. No.: 5.69e-69 Length: 825  
Score: 707.00 Matches: 141  
Percent Similarity: 83.8% Conservative: 24  
Best Local Similarity: 71.6% Mismatches: 30  
Query Match: 21.3% Indels: 2  
Gaps: 2  
DB: 12

US-10-667-289-2 (1-629) x CC496590 (1-825)

QY 434 IleThrGluIleIleGluIlePheIleProGluHisIleProThrAenTyrIleGlyGlu 453  
Db 3 ATTAACAGATTA--GAAATCATTCCTCCCAAGAAAGAAACCTGCGCTCAAGAAAGAA 59

QY 454 ---AsnThrGlyProLeuGluThrArgAspTyrProGlnAenSerLeuPheAspAenThr 472  
Db 60 AACATACAGAGAGCTCGAG 119

QY 473 ThrValValTyrIleProAspLeuAenThrGlyTyrIleProGlnIleSerAenPheLeu 492  
Db 120 ACAGTGTATATTCCTGATCTCAACACTGCGGTATTAACCCAGATTTCAGATTTCCTC 179

C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). "

## ORIGIN

Alignment Scores:	
Pred. No.:	1.85e-65
Score:	673.50
Percent Similarity:	64.4%
Best Local Similarity:	62.3%
Query Match:	20.2%
DB:	7
US-10-667-289-2 (1-629) x BF212748 (1-540)	
	Length: 540
	Matches: 154
	Conservative: 5
	Mismatches: 15
	Indels: 75
	Gaps: 4





DB: 7 Gaps: 0

US-10-667-289-2 (1-629) x BF185326 (1-842)

Qy 479 AppleLeuAnthrGlyTyrLeuProGlnIleSerAphLeuProGlnGlySerHLeu 498  
 |||  
 Db 1 GATCTCAACCTGGATATTAACCCCAATTTCTGCTGAGGAGGACCATCTC 60

Qy 499 SerAphAnthrGlyTyrLeuProGlnIleSerAphLeuProGlnGlySerHLeu 518  
 |||  
 Db 61 AGCATATATATGAAATTAATCTTCTTAACCTTAACACACAGTTGATCTTACTCA 120

Qy 519 GlyAphAnthrProGlnGlyLeuGlnIleProAphAnthrGlnIleSerValSerSerValAph 538  
 |||  
 Db 121 GGAATATATCCAGGTACAAAGCATCTAA-TTCTCTTTCTGTTTCAAGTGAAT 179

Qy 539 SerLeuSerAnthrIlePheLeuGlyGlnLeuSerIleLeuAnthrGlyLeu 558  
 |||  
 Db 180 TCACCTAGACACACATATTTCT-GGAGAAATTAGCCTCATATTAAATCAAGGAAATGC 238

Qy 559 SerSerProAphIleGlnAphSerValGlnGlnIleThrMetLeuLeuGlnAphAnthr 578  
 |||  
 Db 239 AGTTCTCTGACACACAACTCACTAGAGAGGAAACACCATGCT-TTGAAAAATGAT 297

Qy 579 SerProSerGlnThrIleProGlnGlnIleThrLeuLeuProAphGlnIleValSerCysLeu 598  
 |||  
 Db 298 TCACCCAGTAAACTATTTCCAGAACACACCTGCTCTCTGATGAAT-GTCTCTCTGTG- 355

Qy 599 GlyIleValAnthrGlnIleProSerIleAphAnthrThrPheProGlnAnthrIleLeuGln 618  
 |||  
 Db 356 GGGATCGTAATGAGGATTCACATCTATTAATCTTATTTTCCAAAAATAT-TTGAAA 414

Qy 619 SerHisPheAnthrGlySerLeuLeuGlnIle 629  
 |||  
 Db 415 AGCCACTTCATAGATTCACTTGGAAG 447

RESULT 13  
 BF185326 430 bp mRNA linear EST 31-OCT-2000  
 LOCUS 601844139F1 NIH\_MGC\_54 Homo sapiens cDNA clone IMAGE:4064840 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BF185326  
 VERSION BF185326.1 GI:11063769  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 Qy 1 (bases 1 to 430)  
 REFERENCE NIH-MGC http://mgc.nci.nih.gov/  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strauberg, Ph.D.  
 Email: ggaube-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: CLONTECH Laboratories, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.lnl.gov  
 Plate: LNC699 row: n column: 09  
 High quality sequence stop: 388.  
 Location/Qualifiers  
 1..430  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4064840"  
 /tissue\_type="from chronic myelogenous leukemia"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_id="NIH\_MGC\_54"

ORIGIN

Alignment Scores:  
 Pred. No.: 2,7e+40 Length: 430  
 Score: 451.00 Matches: 100  
 Percent Similarity: 69.9% Conservative: 2  
 Best Local Similarity: 68.5% Mismatches: 6  
 Query Match: 13.6% Indels: 39  
 DB: 7 Gaps: 1

US-10-667-289-2 (1-629) x BF185326 (1-430)

Qy 265 TTPAen-ValIyGluPheAphThrAphThrThrValGlnGlnSerGlnPheTyrLe 284  
 |||  
 Db 78 TGGAACGTGTAAGAAATTTGACACCAATTTTACATATGTGCAACAGTCAGAAATTCATCTT 137

Qy 284 UGUProAphAnthrGlyTyrValPheGlnValArgCysGlnGlnIleThrGly-TyrArgTyrT 304  
 |||  
 Db 138 GGAGCCAAACATTAAGTACGTAATTTCAAGTGAAATGTCAGAAACAGGCAAAAGGATCT 197

Qy 304 TPGlnPro-TripSerSer-ProbPhePheIleGlySerThrProGlnThrValProGlnValTh 323  
 |||  
 Db 198 GGACAGCTTAGAGATTGACCGCGTTTTCATATAAACCTGGAACAGTTCCCGAGGTCAC 257

Qy 323 TSerIyValPheGlnHisAphThrThrPheAnthrGlyLeuThrValAlaSerIleSerTh 343  
 |||  
 Db 258 ATCAAAAGCATTCACACATGACACATGAAATTTGGGCTTAAAGTGTTCATCTCTAC 317

Qy 343 TGIyHLeuThrSerAphAnthrGlyAphIleGlyLeuLeuGlnIleValPhe 363  
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 Db 318 AGGGACCTTACTTCT----- 333

Qy 363 eAlaValMetLeuSerIleLeuSerIleGlyIlePheAnthrSerPheAthrGln 383  
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 Db 334 -----GG 335

Qy 383 YIleValArgArgIleLeuLeuLeuIleProIyTTPleuTyrGlnAphIleProAnthr 403  
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 Db 336 ATT-AAAGAGAGATCTTATTTGTAATACCAAGTGGCTTTATGAAGATATCTCATATC 394

Qy 403 LYyAphAnthr 406  
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 Db 395 TGAAAGACCA 404

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 VERSION AO699233.1 GI:5389481  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 Qy 1 (bases 1 to 569)  
 REFERENCE Mellera,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,  
 Kellera,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and  
 Hood,L.



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QY      584  ILeProGluGlnThrLeuLeuProAspGlnPheValSerCysLeuGlyIleValAsnGlu 603
Db      145  ATTCAGAAACAGACCTGCTTCTGATGAATTGTCTCTGTTGGAAATCGATGAG 204
QY      604  GlnLeuProSerIleAsnThrTyrPheProGlnAsnIleLeuGlnSerHisPheAsnArg 623
Db      205  GAGTTGCCATCTATTAACTTATTTCACAAAATATTGAAAGCCACTTCATAGG 264
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Db      265  ATTCACTCTTGAAAAG 282
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Search completed: October 14, 2006, 16:52:19  
Job time : 7930 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OW protein - nucleic search, using frame\_plus.p2n model

Run on: October 14, 2006, 14:25:09 ; Search time 9842 Seconds  
(without alignments)  
6130.298 Million cell updates/sec

Title: US-10-667-289-2

Perfect score: 3326  
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Scoring table:

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 6366136 segs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seg length: 0  
Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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Database :

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12: gb\_hg:.\*  
13: gb\_in:.\*  
14: gb\_cm:.\*  
15: gb\_ba:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3324	99.9	2826	5	AF461422 Homo sapi
2	3324	99.9	2859	2	C0878371 Sequence
3	3324	99.9	2859	2	CS110317 Sequence

4	3324	99.9	2859	2	AR561607	AR561607 Sequence
5	3324	99.9	2859	2	AX338549	AX338549 Sequence
6	3314	99.6	1890	2	AX467350	AX467350 Sequence
7	3314	99.6	1910	2	BD013245	BD013245 Novel hem
8	3314	99.6	2830	2	AX467349	AX467349 Sequence
9	3292	99.0	2123	2	BD013243	BD013243 Novel hem
10	3123	93.9	1779	5	AY937250	AY937250 Homo sapi
11	2952	88.8	1698	2	AX467352	AX467352 Sequence
12	2889	86.9	1676	5	AY937253	AY937253 Homo sapi
13	2889	86.9	1676	5	AY937254	AY937254 Homo sapi
14	2785	83.7	1618	5	AY937251	AY937251 Homo sapi
15	2785	83.7	1618	5	AY937252	AY937252 Homo sapi
16	2764	83.1	1609	5	AY937255	AY937255 Homo sapi
17	2747	82.6	1887	2	AX338551	AX338551 Sequence
18	2284.5	68.7	2488	6	AF461423	AF461423 Mus muscu
19	2280.5	68.6	1935	2	AX467359	AX467359 Sequence
20	2192	65.9	1301	2	BD013244	BD013244 Novel hem
21	2115	65.4	1479	2	BD013242	BD013242 Novel hem
22	2039	61.3	1155	2	AX054989	AX054989 Sequence
23	1902	57.2	1324	5	BC016829	BC016829 Homo sapi
24	1868	56.2	1071	2	AX467354	AX467354 Sequence
25	1747	52.5	1152	2	AX054991	AX054991 Sequence
26	1695	51.0	1784	2	BD013241	BD013241 Novel hem
27	1511	45.4	1532	5	BC040720	BC040720 Homo sapi
28	1122	33.7	122289	5	AL389925	AL389925 Human DNA
29	709	21.3	220412	12	AC167151	AC167151 Bos tauru
30	659	19.8	219288	12	AC111912	AC111912 Rattus no
31	659	19.8	235198	12	AC106822	AC106822 Rattus no
32	659	19.8	236635	12	AC126525	AC126525 Rattus no
33	620	18.6	110000	12	AY657029	AY657029 Contination (4 of
34	620	18.6	181390	6	AC159129	AC159129 Mus muscu
35	620	18.6	216956	6	AC124758	AC124758 Mus muscu
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#### ALIGNMENTS

RESULT 1  
AF461422  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AF461422 2826 bp mRNA linear PRI 29-MAY-2002  
Homo sapiens interleukin-23 receptor (IL-23R) mRNA, complete cds.  
AF461422.1 GI:21239251

REFERENCE  
AUTHORS

1 (bases 1 to 2826)  
Parham,C., Chirica,M., Timans,J., Valseberg,E., Travis,M.,  
Cheung,J., Pflanz,S., Zhang,R., Singh,K.P., Vega,F., To,W.,  
Wagner,J., O'Farrell,A.-M., McClanahan,T., Zurawski,S., Hannum,C.,  
Gorman,D., Rennick,D.M., Kastelein,R.A., de Waal Malefyt,R. and  
Moore,K.W.

A receptor for the heterodimeric cytokine IL-23 is composed of  
IL-12Rbeta1 and a novel cytokine receptor subunit, IL-23R  
J. Immunol. 168 (11), 5699-5708 (2002)

TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS

2 (bases 1 to 2826)  
Parham,C., Chirica,M., Timans,J., Valseberg,E., Travis,M.,  
Cheung,J., Pflanz,S., Zhang,R., Singh,K.P., Vega,F., To,W.,  
Wagner,J., O'Farrell,A.-M., McClanahan,T., Zurawski,S., Hannum,C.,  
Gorman,D., Rennick,D.M., Kastelein,R.A., de Waal Malefyt,R. and  
Moore,K.W.

TITLE Moore,K.W.  
Direct Submission  
JOURNAL Submitted (19-DEC-2001) Immunology, DNA Research, 901 California Ave., Palo Alto, CA 94304, USA

FEATURES  
Source location/Qualifiers

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# ORIGIN

## Alignment Scores:

Prod. No.: 0 Length: 2826  
Score: 3324.00 Matches: 627  
Percent Similarity: 99.7% Conservative: 0  
Best Local Similarity: 99.7% Mismatches: 2  
Query Match: 99.9% Indels: 0  
DB: 5 Gaps: 0

US-10-667-289-2 (1-629) x AF461422 (1-2826)

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DB 1346 AATTAATTCAGAGAGAGAGGCTCTATATGTTGATCCCATGATTAACAAGATTAAGAAATC 1405  
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RESULT 2  
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ACCESSION CQ878371  
VERSION CQ878371.1 GI:53790924  
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ORGANISM Homo sapiens  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
REFERENCE 1  
AUTHORS Olt.M. and Mcclanahan,T.K.  
TITLE Uses of 11-23 agonists and antagonists; related reagents  
JOURNAL Patent: WO 2004081190-A 5 23-SEP-2004;  
SCHERING CORPORATION (US)  
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REFERENCE 1  
 AUTHORS Chirica, M., Kastelein, R. A., Moore, K. W. and Parham, C. L.  
 TITLE 11-23 and its receptor; related reagents and methods  
 JOURNAL Patent: WO 2005052157-A 1 09-JUN-2005;  
 Schering Corporation (US)  
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 AUTHORS Chirica, M., Kaelelein, R. A., Moore, K. W. and Parham, C. L.  
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REFERENCE 1  
 AUTHORS Chirica,M., Kastelein,R.A., Moore,K.W. and Parham,C.L.  
 TITLE Mammalian receptor proteins; related reagents and methods  
 JOURNAL Patent: WO 0185790-A 1 15-NOV-2001;  
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US-10-667-289-2 (1-629) x AK338549 (1-2859)

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RESULT 6  
AX467350



LOCUS AX467350 1890 bp DNA linear PAT 16-JUL-2002  
 DEFINITION Sequence 20 from Patent WO0229060.  
 ACCESSION AX467350  
 VERSION AX467350.1 GI:21900587  
 KEYWORDS  
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 ORGANISM Homo sapiens (human)  
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo.  
 REFERENCE  
 AUTHORS Cosman, D. J., Mosley, B. A., Bird, T. A., Dubose, R. F. and Wiley, S. R.  
 TITLE Hematopoietin receptors hpr1 and hpr2  
 JOURNAL Patent: WO 0229060-A 20 11-APR-2002;  
 Immunex Corporation (US)  
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Oy	601	ValenGIuGIuLeuProSerIIeAsnThrYyrPheProGIuAnIIleleuGIuSerHis	620
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Oy	621	PheAsnArgIIleSerIIeLeuGIuLys	629
Dd	1861	TTCATAGGATTTCACTCTTGAAAAAG	1887
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DEFINITION	Novel hemopoietin receptor protein, NR12.		
VERSION	BD013245		
KEYWORDS	BD013245.1 GI:22093434 WO 0133556-A/5. Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 1910) Maeda,M. and Yaguchi,N. Novel hemopoietin receptor protein, NR12 Patent: WO 0123556-A 5 05-Apr-2001; CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE INC. ASATSUGU MAEDA, NORIKO YAGUCHI OS Homo sapiens (human) PN WO 0123556-A/5 PD 05-APR-2001 PF 27-SEP-2000 WO 2000JP006654 PR 27-SEP-1999 JP 99P 273358, 03-AUG-2000 JP OOP 240397 PI MASATSUGU MAEDA,NORIKO YAGUCHI PC C12N15/12,C12N1/21,C12N5/10,C07K14/715,C07K16/28,C12P21/02, G0N133/567		
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US-10-667-289-2 (1-629) x BD013245 (1-1910)			
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RESULT 8
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LOCUS AX467349 Sequence 19 from Patent WO0229060.
DEFINITION AX467349
ACCESSION AX467349
VERSION AX467349.1 GI:21900586
KEYWORDS
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ORGANISM Homo sapiens
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            Homiidae; Homo.
REFERENCE
1 Cosman,D.J., Mosley,B.A., Bird,T.A., Dubose,R.F. and Wiley,S.R.
  Hematopoietic receptors hpx1 and hpx2
  Patent: WO 0229060-A 19 11-APR-2002;
  Immunex Corporation (US)
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Qy      41 11ePheLeuMetG1yMetAsn11eSer11eTyrCysG1uAlaAla11eLeuAsnCysG1n 60
Db      227 ATTTTAAGATGGATGATGAATATCTCTATATATTCGCAAGCAGCAATTAAGACCTGCAA 286
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 SOURCE Homo sapiens (human)  
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 1 (bases 1 to 2123)  
 REFERENCE  
 AUTHORS Maeda,M. and Yaguchi,N.  
 TITLE Novel hemopoietin receptor protein, NR12

JOURNAL Patent: WO 0123556-A 3 05-APR-2001;  
 CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE INC, ASATSUGU  
 MAEDA, NORIKO YAGUCHI  
 COMMENT OS Homo sapiens (human)  
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 PD 05-APR-2001  
 PR 27-SEP-2000 WO 2000/006654  
 PR 27-SEP-1999 JP 99P 273358, 03-AUG-2000 JP 00P 240397 PI  
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LOCUS        Homo sapiens interleukin 23 receptor isoform 1 mRNA, partial cde,
DEFINITION   alternatively spliced.
VERSION      AY937250
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SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 1779)
Zhang, X.-Y., Zhang, H.-J., Zhang, Y., Fu, Y.-J., He, J., Zhu, L.-P.,
Wang, S.-H. and Liu, L.
Identification and expression analysis of alternatively spliced
isoforms of human interleukin-23 receptor gene in normal lymphoid
cells and selected tumor cells
Immunogenetics 57 (12), 934-943 (2006)
16372191
JOURNAL      PubMed
PUBMED       2 (bases 1 to 1779)
Zhang, X.-Y., Zhang, Y., Wang, S.-H. and Liu, L.
Direct Sublation
Submitted (16-FEB-2005) Microbiology and Etiology, Peking Union
Medical College, #5 Dong Dan San Tiao, Beijing 100005, China
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US-10-667-289-2 (1-629) x AY937250 (1-1779)

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 Db 901 ACGATGCTTCCATCTCTACAGGCGACCTTACTTGACAAACAGAGAGACATTTGACCTT 960  
 QY 357 LeuLeuGluMetIleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePhe 376  
 Db 961 TTTTGGGAATGATCGCTTCTGTTATATTTGTCATTTCTTTGATGGGATATTT 1020  
 QY 377 AsnArgSerPheArgThrGlyIleLysArgArgIleLeuLeuLeuIleProLysTrpLeu 396

Db 1021 AACAGATCATCCGAACTGGGATTTAAAGAGAGATCTTGTTAAATACCAAGTGGCTT 1080  
 QY 397 TyrGluAspIleProAsnMetLysAsnSerAsnValValLysMetLeuGlnIleAsnSer 416  
 Db 1081 TATGAAGATATTTCTTAATATGAAAAACACACATGTTGTGAAAAATGCTACAGAAATAGT 1140  
 QY 417 GluLeuMetAsnAsnAsnSerSerGluGlnValLeuTyrValAspProMetIleThrGlu 436  
 Db 1141 GAACCTATGAATATATATCCAGTGAGAGGTCCTATATGTTGATCCCATGATTAACAGAG 1200  
 QY 437 IleLysGluIlePheIleProGlnHisLysProThrAspTyrTyrLysGluAsnThrGly 456  
 Db 1201 ATAAAAAATATCTTCAATCCAGAACCAAGCCCTACAGCTACCAAGAGAAATACAGGA 1260  
 QY 457 ProLeuGluThrArgAspTyrProGlnAsnSerLeuPheAspAsnThrThrValIleTyr 476  
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RESULT 11  
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 DEFINITION Sequence 22 from Patent WO0229060.  
 AX467352  
 ACCESSION AX467352  
 VERSION AX467352.1 GI:21900588  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.

REFERENCE  
 1 Cosman, D.J., Mosley, B.A., Bird, T.A., Dubose, R.F. and Wiley, S.R.  
 Hematopoietic receptors hprt and hprt2  
 Patent: WO 0229060-A 22 11-APR-2002;  
 ImmuneX Corporation (US)  
 Location/Qualifiers  
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FEATURES  
 source  
 ORIGIN

## Alignment Scores:

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Percent Similarity:	89.3%	Conservative:	0
Best Local Similarity:	89.3%	Mismatches:	3
Query Match:	88.8%	Indels:	64
DB:	2	Gaps:	1

US-10-667-289-2 (1-629) x AX467352 (1-1698)

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QY      21 CyHhIsgIyGlyIleThrAenIleAenCySerGlyVHlIleTrpValGluProAlaThr 40
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QY      41 IlePheLysMetGlyMetAenIleSerIleTrpCySerGlnAlaIleLysAenCySerGln 60
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DB      121 ATTTTAAAGATGGGTATGAAATATCTCTATATTTGCCAAGCACCAATTAGAACTGCCAA 180
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DB      951 ----- 951
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DB      1069 AATTAATTCAGTGAAGAGGTCTTATATGTGTGATCCCATATTAACAGATTAAGAAATC 1128
QY      441 PheIleProGluHlsLysProThrAspTrpLysLysGluAsnThrGlyProLeuGluThr 460
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QY      561 ProAspIleGlnAsnSerValGluGluGluThrThrMetLeuLeuGluAsnAspSerPro 580
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QY      601 ValAsnGluGluLeuProSerIleAenThrTrpPheProGluAsnIleLeuGluSerHls 620
DB      1609 GTGAATGAGAGATGTCATTAATTAATCTTATTTTCCCAAAATATTTTGGAAAAACAC 1668
QY      621 PheAsnArgIleSerLeuLeuLys 629
DB      1669 TTCAATATGATTTCACTTGGAAAAAG 1695

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## RESULT 12

AY937253 1676 bp mRNA linear PRI 07-FEB-2006  
 LOCUS Homo sapiens interleukin 23 receptor isoform 3 FI mRNA, partial  
 DEFINITION cds, alternatively spliced.  
 ACCESSION AY937253  
 VERSION AY937253.1 GI:62870704





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Qy 537 ValAsnSerLeuSerAnthrIlePheLeuGlyGluLeuSerLeuIleLeuAnGlnGly 556
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Qy 577 AsnAspSerProSerGluThrIleProGluGlnThrLeuLeuProArgIlePheValSer 596
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Qy 597 CysLeuGlyIleValAnGluGluLeuProSerIleAnThrTyPheProGlnAsnIle 616
Db 1578 TGTTGGGAGATCGGAATGAGAGAGTTGCCATCTATTAATCTTATTTCCACAAATATTT 1637
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RESULT 13
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LOCUS AY937254
DEFINITION Homo sapiens interleukin 23 receptor isoform 3 F3 mRNA, partial
cde, alternatively spliced.
ACCESSION AY937254
VERSION AY937254.1 GI:62870706
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 1676)
Zhang,X.Y., Zhang,H.J., Zhang,Y., Fu,Y.J., He,J., Zhu,L.P.,
Wang,S.H. and Liu,L.
Identification and expression analysis of alternatively spliced
isoforms of human interleukin-23 receptor gene in normal lymphoid
cells and selected tumor cells
Immunogenetics 57 (12), 934-943 (2006)
16372191
2 (bases 1 to 1676)
Zhang,X.-Y., Zhang,Y., Zhang,H.-J., Wang,S.-H. and Liu,L.
Direct Submision
Submitted (16-FEB-2005) Microbiology and Etiology, Peking Union
Medical College, #5 Dong Dan San Tiao, Beijing 100005, China
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DB 1578 TGTTTGGGAGATCGGATAGAGAGGTTGCCATCTATTAATCTTATTTTCCACAAATATT 1637  
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DB 1638 TTGGAAGCCACTTCATAGATTCTCTTGGAAGAAG 1676  
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DEFINITION Homo sapiens interleukin 23 receptor isoform 2 fl mRNA, partial  
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ACCESSION AY937251  
VERSION AY937251.1 GI:62870700  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.

REFERENCE 1 (bases 1 to 1618)  
AUTHORS Zhang,X.Y., Zhang,H.J., Zhang,Y., Fu,Y.J., He,J., Zhu,L.P.,  
Wang,S.H. and Liu,L.  
TITLE Identification and expression analysis of alternatively spliced  
isoforms of human interleukin-23 receptor gene in normal lymphoid  
cells and selected tumor cells  
JOURNAL Immunogenetics 57 (12), 934-943 (2006)  
PUBMED 16372191  
REFERENCE 2 (bases 1 to 1618)  
AUTHORS Zhang,X.-Y., Zhang,Y., Wang,S.-H. and Liu,L.  
TITLE Direct Submission  
JOURNAL Submitted (16-FEB-2005) Microbiology and Etiology, Peking Union  
Medical College, #5 Dong Dan San Tiao, Beijing 100005, China  
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DEFINITION cds, alternatively spliced.
ACCESSION AY937252
VERSION AY937252.1 GI:62870702
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Zhang,X.-Y., Zhang,H.J., Zhang,Y., Fu,Y.J., He,J., Zhu,L.P.,
Wang,S.H. and Liu,L.
TITLE Identification and expression analysis of alternatively spliced
isoforms of human interleukin-23 receptor gene in normal lymphoid
cells and selected tumor cells
JOURNAL Immunogenetics 57 (12), 934-943 (2006)
PUBMED 16372191
REFERENCE
AUTHORS Zhang,X.-Y., Zhang,H.J., Zhang,Y., Wang,S.-H. and Liu,L.
TITLE Direct Submision
JOURNAL Submitted (16-FEB-2005) Microbiology and Etiology, Peking Union
Medical College, #5 Dong Dan San Tiao, Beijing 100005, China
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ORIGIN
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US-10-667-289-2 (1-629) x AY937252 (1-1618)

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Run on: October 14, 2006, 12:54:04 ; Search time 518 Seconds  
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Listing first 45 summaries

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#### SUMMARIES

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4	253.4	8.9	144034	US-09-949-001-35	Sequence 35, Appl1
5	253.4	8.9	601	US-09-949-001-581	Sequence 581, Appl1
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#### ALIGNMENTS

RESULT 1  
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Sequence 1, Application US/09853180B  
Patent No. 6756481  
GENERAL INFORMATION:  
APPLICANT: Chirica, Madeline  
APPLICANT: Parham, Christi L.  
APPLICANT: Kastelein, Robert A.  
APPLICANT: Moore, Kevin W.  
TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods.  
FILE REFERENCE: DX01074  
CURRENT APPLICATION NUMBER: US/09/853,180B  
CURRENT FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: 60/203,426  
PRIOR FILING DATE: 2000-05-10  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1  
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ORGANISM: Homo sapiens  
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FEATURE:  
NAME/KEY: misc feature  
LOCATION: (127)..(127)  
OTHER INFORMATION: k means g or t/u. See page 12, line 34, of patent application as  
OTHER INFORMATION: originally filed.  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: (188)..(2005)  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (563)..(563)  
OTHER INFORMATION: t means g or a. See page 12, line 36, of patent application as  
OTHER INFORMATION: originally filed.  
US-09-853-180B-1

Query Match 100.0%; Score 2857.4; DB 3; Length 2859;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2859; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 541 CATGACTTGCACCTGGAATCTGGAAGCTCACTCATAGACACAAATATCGTGTACA 600  
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Db 541 CATGACTTGCACCTGGAATCTGGAAGCTCACTCATAGACACAAATATCGTGTACA 600  
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QY 601 TGTGAAGAGTTTGAAGACAGAGAGAGCAACAGTATCTCACTCAAGCTATATTAACAT 660  
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|  
|  
Db 601 TGTGAAGAGTTTGAAGACAGAGAGAGCAACAGTATCTCACTCAAGCTATATTAACAT 660  
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|  
QY 661 CTCACCTGATTTCTTAAAGGTGGCAAGAGTACTTGGTTTGGTCCAAACAGGAAACGC 720  
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|  
|  
Db 661 CTCACCTGATTTCTTAAAGGTGGCAAGAGTACTTGGTTTGGTCCAAACAGGAAACGC 720  
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|  
QY 721 ACTAGGATGGAAGAGTCAAAACAATGCAAAATTCACCTGGAATGATATGATACCTTC 780  
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|  
Db 721 ACTAGGATGGAAGAGTCAAAACAATGCAAAATTCACCTGGAATGATATGATACCTTC 780  
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QY 781 TGCAGCCGTCAATTCAGGGCTGAGACTATTAATGCTACAGTGCCTCAAGCAACATATTTA 840  
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|  
Db 781 TGCAGCCGTCAATTCAGGGCTGAGACTATTAATGCTACAGTGCCTCAAGCAACATATTTA 840  
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QY 841 TTGGGAATGTCAAACAACAATGAAAAGTTTCTGTGAAATGAGATCAAGGCTTAAC 900  
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Db 841 TTGGGAATGTCAAACAACAATGAAAAGTTTCTGTGAAATGAGATCAAGGCTTAAC 900  
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QY 901 AAACCAAACTTGGAAATGTTAAAGAAATTTGACACCAATTTTACATATGCAACAGTCAGA 960  
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|  
|  
Db 901 AAACCAAACTTGGAAATGTTAAAGAAATTTGACACCAATTTTACATATGCAACAGTCAGA 960  
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QY 961 ATTCTACTTGAAGCAAACTTAAGTACGTAATTTCAAGTGAATGTCAGAAACAGGCAA 1020  
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Db 961 ATTCTACTTGAAGCAAACTTAAGTACGTAATTTCAAGTGAATGTCAGAAACAGGCAA 1020  
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QY 1021 AAGGTACTGAGCACTTGAAGTTCACCGTTTTTTTCAAAAAACCTGAAACAGTTTCCCA 1080  
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Db 1021 AAGGTACTGAGCACTTGAAGTTCACCGTTTTTTTCAAAAAACCTGAAACAGTTTCCCA 1080  
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QY 1081 GGTCACTCAAAAGCAATTCACAATGACATGAAATTTCTGGGCTTAACAGTTGCTTCAT 1140  
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Db 1081 GGTCACTCAAAAGCAATTCACAATGACATGAAATTTCTGGGCTTAACAGTTGCTTCAT 1140  
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QY 1141 CTCTACAGGGACACTTACTTCTGACACACAGAGAGACATTTGACCTTTATTTGGGAATGAT 1200  
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Db 1141 CTCTACAGGGACACTTACTTCTGACACACAGAGAGACATTTGACCTTTATTTGGGAATGAT 1200  
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QY 1201 CGTCTTGTGCTGTTATGTTGTCATATCTTCTTGTGATTTGGGATTTTAAACATCATTCG 1260  
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Db 1201 CGTCTTGTGCTGTTATGTTGTCATATCTTCTTGTGATTTGGGATTTTAAACATCATTCG 1260  
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QY 1261 AACTGGATTTAAAGAAAGATCTTAATGTTAATACCAAGTGGCTTTATGAAATATTC 1320  
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Db 1261 AACTGGATTTAAAGAAAGATCTTAATGTTAATACCAAGTGGCTTTATGAAATATTC 1320  
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Db 1321 TAAATGAAAAACAGCAATTTGTGAAATATGCTACAGAGAAATATGTAACCTTATGAAATTA 1380  
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QY 1381 TAAATTCAGTGAAGCAGGTCTTATATGTTATATCCATGATTAACAGAGATTAAGAAATCTT 1440  
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Db 1381 TAAATTCAGTGAAGCAGGTCTTATATGTTATATCCATGATTAACAGAGATTAAGAAATCTT 1440  
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QY 1441 CATCCGAGAACACAGCTTACAGACTTACAGAAAGAGAAATACAGACCCCTGAGACAA 1500  
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Db 1441 CATCCGAGAACACAGCTTACAGACTTACAGAAAGAGAAATACAGACCCCTGAGACAA 1500  
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QY 1501 AGACTACCCGCAAACTCGCTATTTCCAGCAATACACAGTTGTATATTTCTGATCTCA 1560  
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Db 1501 AGACTACCCGCAAACTCGCTATTTCCAGCAATACACAGTTGTATATTTCTGATCTCA 1560  
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QY 1561 CACTGATATTAACCCCAAAATTTCAATTTTCTGCTGAGAGAGAACCATCTCAGCAATA 1620  
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Db 1561 CACTGATATTAACCCCAAAATTTCAATTTTCTGCTGAGAGAGAACCATCTCAGCAATA 1620  
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QY 1621 TAAATGAATTAATCTTCTTAAACACTTAAACCAAGTTGATTTCTTGAATCTCAGAAATA 1680  
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Db 1621 TAAATGAATTAATCTTCTTAAACACTTAAACCAAGTTGATTTCTTGAATCTCAGAAATA 1680  
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QY 1681 TCCCAAGTTACAAAAGATCTCTAATTTTGTGTTTCTGTTCAAGTGTGAATTCATGA 1740  
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Db 1681 TCCCAAGTTACAAAAGATCTCTAATTTTGTGTTTCTGTTCAAGTGTGAATTCATGA 1740  
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QY 1741 CAACACAATATTTCTTGAAGAAATTAAGCCCTCATATTAATCAAGAGAAATGCAAGTTCTCC 1800  
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Db 1741 CAACACAATATTTCTTGAAGAAATTAAGCCCTCATATTAATCAAGAGAAATGCAAGTTCTCC 1800  
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QY 1801 TGAATACAAAACCTCAGTAGAGAGAGAAACCAACATGCTTTTGAATAATGATTCACCCAG 1860  
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Db 1801 TGAATACAAAACCTCAGTAGAGAGAGAAACCAACATGCTTTTGAATAATGATTCACCCAG 1860  
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QY 1861 TGAATCTATTTCCAGAACAGACCCCTGCTCTGATGAAATTTGTCTCTGTTTGGGATCGT 1920  
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Db 1861 TGAATCTATTTCCAGAACAGACCCCTGCTCTGATGAAATTTGTCTCTGTTTGGGATCGT 1920  
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QY 1921 GAATGAGAGTGGCATCTATTAATCTTATTTTCCACAAATATTTTGGAAAGCACTT 1980  
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Db 1921 GAATGAGAGTGGCATCTATTAATCTTATTTTCCACAAATATTTTGGAAAGCACTT 1980  
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|  
QY 1981 CAATAGATTTCACTTGTGAAAAATGAGCTGTGTGTCAAAATCAATATGAGAAAGCT 2040  
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Db 1981 CAATAGATTTCACTTGTGAAAAATGAGCTGTGTGTCAAAATCAATATGAGAAAGCT 2040  
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QY 2041 GCCTTGCAATCTGAACCTTGGGTTTTCCCTGCAATAGAAATTTGAATTTCTGCTCTTTTGA 2100  
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Db 2041 GCCTTGCAATCTGAACCTTGGGTTTTCCCTGCAATAGAAATTTGAATTTCTGCTCTTTTGA 2100  
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QY 2101 AAAAAATGTAATTCACATACAAATCTTCACTGACATGCAATGTTTCAATTCCTTGAATA 2160  
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|  
Db 2101 AAAAAATGTAATTCACATACAAATCTTCACTGACATGCAATGTTTCAATTCCTTGAATA 2160  
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QY 2161 ATACTAGTGAAGGAGATTTGCTGGGCCATATGATTAAGCATATGTTTCAAGTTCTCAATCT 2220  
|  
|  
|  
Db 2161 ATACTAGTGAAGGAGATTTGCTGGGCCATATGATTAAGCATATGTTTCAAGTTCTCAATCT 2220  
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|  
QY 2221 TGTTCACAGATGATGACATTTCTGTGCTCTTACATCAACATGTAAGAAATTCCTGGGAG 2280  
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QY 2547 AAATAGAAATCATTTAGGCGGCGGCTGGCTCATCTGTAAATCCAGACATTTGGTAG 2606
DB 69679 AAATAGCAAAATTTTGGCCGGGCGATGGTGGCTCACCCCTGTAGTCCAGACATTTGGTAG 69738
QY 2607 GCGAGGTGGTGGATCACTGAGGTCAAGAGTTGAGTCCAGCTGGCCCAATATGCTGA 2666
DB 69739 GCGAGGTGGTGGATCACTGAGGTCAAGAGTTGAGTCCAGCTGGCCCAATATGCTGA 69798
QY 2667 AACCTGTCTCTACTAAATTTAGCCGCGCATGTGGAGGTGCTGTATATC 2726
DB 69799 AACCTGTCTCTACTAAATTTAGCCGCGCATGTGGAGGTGCTGTATATC 69858
QY 2727 CCAGCTACTTGGAGGCTGAGGCGAGAGATCACTTGAACGAGAAAGGAGAGTTGGAC 2786
DB 69859 CCAGCTACTTGGAGGCTGAGGCGAGAGATCACTTGAACCTGGAGGTGGAGTTGGAC 69918
QY 2787 TGAGCTGAGATTGTGCGACCTGCACTCCAGCTGGGCAAGAGCAAACTGTGTCTGA 2846
DB 69919 TGAGCTGAGATTGTGCGACCTGCACTCCAGCTGGGCAAGAGCGAAACTGTGTCTCAA 69978
QY 2847 AAAAAAAAAAAAAA 2859
DB 69979 AAAAAAAAAAAAAA 69991

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## RESULT 4

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US-09-949-001-35
; Sequence 35, Application US/09949001
; Patent No. 6825336
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL000789
; CURRENT APPLICATION NUMBER: US/09/949,001
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/231,323
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 144034
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc_feature
; LOCATION: (1)..(144034)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-001-35

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Query Match 8.9%; Score 253.4; DB 3; Length 144034;

Best Local Similarity 87.9%; Pred. No. 5.5e-57;

Matches 275; Conservative 1; Mismatches 37; Indels 0; Gaps 0;

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QY 2547 AAATAGAAATCATTTAGGCGGCGGCTGGCTCATCTGTAAATCCAGACATTTGGTAG 2606
DB 69679 AAATAGCAAAATTTTGGCCGGGCGATGGTGGCTCACCCCTGTAGTCCAGACATTTGGTAG 69738
QY 2607 GCGAGGTGGTGGATCACTGAGGTCAAGAGTTGAGTCCAGCTGGCCCAATATGCTGA 2666
DB 69739 GCGAGGTGGTGGATCACTGAGGTCAAGAGTTGAGTCCAGCTGGCCCAATATGCTGA 69798
QY 2667 AACCTGTCTCTACTAAATTTAGCCGCGCATGTGGAGGTGCTGTATATC 2726
DB 69799 AACCTGTCTCTACTAAATTTAGCCGCGCATGTGGAGGTGCTGTATATC 69858
QY 2727 CCAGCTACTTGGAGGCTGAGGCGAGAGATCACTTGAACGAGAAAGGAGAGTTGGAC 2786
DB 69859 CCAGCTACTTGGAGGCTGAGGCGAGAGATCACTTGAACCTGGAGGTGGAGTTGGAC 69918
QY 2787 TGAGCTGAGATTGTGCGACCTGCACTCCAGCTGGGCAAGAGCAAACTGTGTCTGA 2846
DB 69919 TGAGCTGAGATTGTGCGACCTGCACTCCAGCTGGGCAAGAGCGAAACTGTGTCTCAA 69978

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QY 2847 AAAAAAAAAAAAAA 2859
DB 69979 AAAAAAAAAAAAAA 69991

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## RESULT 5

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US-09-949-001-581
; Sequence 581, Application US/09949001
; Patent No. 6825336
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL000789
; CURRENT APPLICATION NUMBER: US/09/949,001
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/231,323
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 581
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-001-581

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Query Match 8.9%; Score 253; DB 3; Length 601;

Best Local Similarity 87.5%; Pred. No. 5.6e-58;

Matches 274; Conservative 2; Mismatches 37; Indels 0; Gaps 0;

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QY 2547 AAATAGAAATCATTTAGGCGGCGGCTGGCTCATCTGTAAATCCAGACATTTGGTAG 2606
DB 122 AAATAGCAAAATTTTGGCCGGGCGATGGTGGCTCACCCCTGTAGTCCAGACATTTGGTAG 181
QY 2607 GCGAGGTGGTGGATCACTGAGGTCAAGAGTTGAGTCCAGCTGGCCCAATATGCTGA 2666
DB 182 GCGAGGTGGTGGATCACTGAGGTCAAGAGTTGAGTCCAGCTGGCCCAATATGCTGA 241
QY 2667 AACCTGTCTCTACTAAATTTAGCCGCGCATGTGGAGGTGCTGTATATC 2726
DB 242 AACCTGTCTCTACTAAATTTAGCCGCGCATGTGGAGGTGCTGTATATC 301
QY 2727 CCAGCTACTTGGAGGCTGAGGCGAGAGATCACTTGAACGAGAAAGGAGAGTTGGAC 2786
DB 302 CCAGCTACTTGGAGGCTGAGGCGAGAGATCACTTGAACCTGGAGGTGGAGTTGGAC 361
QY 2787 TGAGCTGAGATTGTGCGACCTGCACTCCAGCTGGGCAAGAGCAAACTGTGTCTGA 2846
DB 362 TGAGCTGAGATTGTGCGACCTGCACTCCAGCTGGGCAAGAGCGAAACTGTGTCTCAA 421
QY 2847 AAAAAAAAAAAAAA 2859
DB 422 AAAAAAAAAAAAAA 434

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## RESULT 6

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US-09-949-016-162811/c
; Sequence 162811, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08

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; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 162811
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; OS: 949-016-162811
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Query Match	8.8%	Score 252.8;	DB 3;	Length 601;
Best Local Similarity	83.5%;	Pred. No. 6.3e-58;		
Matches 284; Conservative	2;	Mismatches 54;	Indels 0;	Gaps 0;

Qy	2520	TAAATATAATCTGAAAATTTTCCCTTTAAATAGATCATTTAGCCAGCGCTGGGCTC	2579
Db	400	TCAGAAAATATCCCAATTGGGGCTTTGAAAAGAAAAGAAAAGTGGGGTGTGGGCTC	341
Qy	2580	ATGCTTTGAATCCCAAGCATTTTGGTAGCTGAGGTGGTGGATCATCCTGAGGTCAAGAGT	2633
Db	340	ATGCGCTGTAAATCCACAGCATTTTGGAGGGCCAGAGGTGGGCRATGACCTGAGGTCAAGAGT	281
Qy	2640	TCGAGTCCAGCCTGGCCAAATATGCTGAAGAACCTGTCTCTACTAAATATACAAAATTAGC	2699
Db	280	TCGAAACCGAGCTGGCCAAACATGGTGAATACCCCGTCTCTACTAAATATACAAAATTAGC	221
Qy	2700	CGGCGATGTGGCAGGTGCTTGTATATCCAGCTACTTTGGAGGCTGAGGCAAGAAATCA	2755
Db	220	TGGGCACTGTGACAGGCGCCCTGTATATCCACGCTACTTTGGAGGCTGAGGCAAGAAATCA	161
Qy	2760	CTTGAACCAAGAAAGGCAGAGGTGTCATCGAGCTGAGATTGTGCCACTGCACTCCAGCCTG	2819
Db	160	CTTGAACCCGGGAAGCGAGGTGTCAGTGAAGCGAGATTGTGCCATTGCACTCCAGCCTG	101
Qy	2820	GGCAACAAAGACAAATCTGTCTTGAAAAAATTTTTTTTTT	2859
Db	100	GGGACAAAGACAAAGACTTGTCTTCAAAAAAATTTTTT	61

RESULT 7  
US-09-949-016-15964/C  
; Sequence 15964, Application US/09949016

? Patent No.6812339  
 ? GENERAL INFORMATION:  
 ? APPLICANT: VENTER, J. Craig et al.  
 ? TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ? TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ? FILE REFERENCE: CLO01307  
 ? CURRENT FILING DATE: US/09/949,016  
 ? CURRENT FILING DATE: 2000-04-14  
 ? PRIOR APPLICATION NUMBER: 60/241,755  
 ? PRIOR FILING DATE: 2000-10-20  
 ? PRIOR APPLICATION NUMBER: 60/237,768  
 ? PRIOR FILING DATE: 2000-10-03  
 ? PRIOR APPLICATION NUMBER: 60/231,498  
 ? PRIOR FILING DATE: 2000-09-08  
 ? NUMBER OF SEQ ID NOS: 207012  
 ? SOFTWARE: FastSeq for Windows Version 4.0  
 ? SEQ ID NO 15964  
 ? LENGTH: 90618  
 ? TYPE: DNA  
 ? ORGANISM: Human  
 ? US-09-949-016-15964

Query Match	8.8%	Score 252.4;	DB 3;	Length 90618;
Best Local Similarity	85.4%	Pred. No. 8.2e-57;		
Matches 280;	Conservative 1;	Mismatches 47;	Indels 0;	Gaps 0;

Qy	Db	Qy	Db
2532	TGAAATTTTCCTTTAAATAGATCATTTGGCCAGGCGCGTGGGCTCATGCTGTAAATC	2591	
72673	TTTATTAATTTGCATTAAATGTATTAAGTAAACAGCGCGGCGCGGTGCTCATGCTGTAAATC	726147	
2592	CCAGCATCTTTGGTATGCGCTGAGGTGGTGATCACTTGAGTTCAGGAGTTTGAGTCCAGCC	2651	
72613	CCAGCATCTTTGGAGAGGCCAAGGCGGGGTGGATCACTTGAGGTTCAGGAGTTTGAGAACACAGCC	72554	

Accession	Sequence	Position
QY	2852 TGGCAATATGCTGAAACCTGTCTCTACTAAATATGCAAAATTTAGCGGCAATGTGTG	2711
Db	72553 TGGCAACATGCGGAAACCTGTCTCTACTAAATATGCAAAATTTAGCGGCAATGTGTG	72499
QY	2712 CAGGTGCTTGTAAATCCAGCTACTTTGGAGGCTGAGGCAAGAGAAATCATTTGAACCGAGA	2771
Db	72493 CAGGCGCTGTAAATCCAGCTACTTCGGAGGCGTAAACAGAGAAATCGCTTGAACCTGGG	72433
QY	2772 AGGCAAGGTTGCACTGAGCTGAGATTGTGCCACTGCACTCCAGCTGGGCAACAGAGC	2831
Db	72433 AGGCAAGGTTGCACTGAGCTGAGATTGTGCCACTTCCAGCTGGGCAACAGAGC	72374
QY	2832 AAAACTCTGCTGAAAAAATTTAAAAA	2859
Db	72373 GAGACTTCATCTCAAAAAAATTTAAAAA	72346

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RESULT 8
US-09-949-016-70153
; Sequence 70153, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 70153
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-70153

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Query Match	8.8%	Score 252;	DB 3;	Length 601;
Best Local Similarity	83.9%	Pred. NO. 1e-57;		
Matches 282; Conservative	2;	Mismatches 52;	Indels 0;	Gaps 0;

Oy	2518	AGTAAATAATAGCTGAAAATTTTCCCTTTAAATAGATCATTAAGGCGAGCGGTGGC	2577
Db	82	AGTAAATGCAATATTCGACTTTTTCGATCAAAGAATATGGCAAGCGCAGCGGTGGC	141
Oy	2578	TCATGCTTGTAAATCCACGACCTTTGGTAGGCTGAGTGGGTGATCACTGAGGTCA	2637
Db	142	TCAGTCTGTAAATCCACGACCTTTGGAGGCGCAGGCGATGATCACTGAGGTCA	201
Oy	2638	GTTGCAGTCCAGCTGGCGCAATATGCTGAACCTGTCTCTACTTAAATATTA	2697
Db	202	GTTGCAACCACTCTGGCCAACTGTGTAAACCCCGTCTTACTTAAATATTA	261
Oy	2698	GCCGCGCATGCTGGCAAGTCTTGTAAATCCAGCTACTTGGAGGCTGAGGCA	2757
Db	262	GCTGGGGGTGTGGCAACGCGCTGTATTAACACTACTTCGAGGCGTGAAGCGAGAAAT	321
Oy	2758	CACTTGAACAGGAAGGACAGAGTGTGACGTGAGCTGATTTGSCACTGCACTCCAGCC	2817
Db	322	CGCTTGAACCTGGGAGGCAAGGTTGCAAGTGAAGTCTGTCCACTTCGACTCCAGCC	381
Oy	2818	TGGGCAACAGAGCAAACTCTGTCTGGAAAAAAA	2853
Db	382	TGGGCAATAGAGCAAACTCTGTCTCAAAAAATA	417

## RESULT 9

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US-09-949-016-16296/c
; Sequence 16296, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 16296
; LENGTH: 49301
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(49301)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16296

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Query Match      8.8%; Score 251.6; DB 3; Length 49301;
Best Local Similarity 83.5%; Pred. No. 1e-56;
Matches 284; Conservative 1; Mismatches 55; Indels 0; Gaps 0;

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QY 2520 TAAATATATATGCTGAAATTTTCCCTTAAATATGATCATTAAGCCAGGCGTGGTGC 2579
DB 9585 TCAAGAAATATATATCCCTTTGGGGCTTTGAAAGAAAGAAAGTCCGGGTGTGCTC 9526
QY 2580 ATGCTGTATATCCAGACCTTTGTAGTCTGAGGTGTGATCACTGAGTCAAGAGT 2639
DB 9525 ATGCTGTATATCCAGACCTTTGTAGTCTGAGGTGTGATCACTGAGTCAAGAGT 9466
QY 2640 TCGAGTCCAGCTTCGCGCAATATGCTGAAACCTCTCTACTAATAATTAATAATTAAT 2699
DB 9465 TCGAAACCAACCTTCGCGCAATATGCTGAAACCTCTCTACTAATAATTAATAATTAAT 9406
QY 2700 CGGCGATGTGGCGAGGTGCTTTGATCCAGACTACTTGGAGGCTGAGGAGAGATCA 2759
DB 9405 TGGGCAAGGTGGCGAGGCTCTGATCCAGCTACTTGGAGGCTGAGGAGAGATCA 9346
QY 2760 CTGAAACCAAGAGGAGGCTTGCATGAGCTGAGATTGTGCCACTGCACTCCAGCTG 2819
DB 9345 CTGAAACCCGGGAGGCGAGGCTTGCATGAGCTGAGATTGTGCCACTGCACTCCAGCTG 9286
QY 2820 GGCAACCAAGAGCAAACTCTGCTGGAGAAAAAATTAATTAATTAATTAATTAATTAAT 2859
DB 9285 GGGAACCAAGAGCAAACTCTGCTGGAGAAAAAATTAATTAATTAATTAATTAATTAAT 9246

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RESULT 10
US-09-949-016-13807
; Sequence 13807, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

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; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 13807
; LENGTH: 168971
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(168971)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13807

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Query Match      8.8%; Score 250.8; DB 3; Length 168971;
Best Local Similarity 83.9%; Pred. No. 2.9e-56;
Matches 282; Conservative 1; Mismatches 53; Indels 0; Gaps 0;

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QY 2518 AGTAAATATATGCTGAAATTTTCCCTTAAATATGATCATTAAGCCAGGCGTGGTGC 2577
DB 164083 AGTAAATGCAATATGCAATTTTGTCTATCAAAAGTAAATGCAAGGCCAGGCGTGGTGC 164142
QY 2578 TCAATGCTGTATATCCAGACCTTTGTAAGGCTGAGGTGATGATCACTGAGTCAAGA 2637
DB 164143 TCAATGCTGTATATCCAGACCTTTGTAAGGCTGAGGTGATGATCACTGAGTCAAGA 164202
QY 2638 GTTGAAGTCCAGGCTGCGCAATATGCTGAAACCTGTCTCTACTAATAATTAATAATTA 2697
DB 164203 GTTGAAGTCCAGGCTGCGCAATATGCTGAAACCTGTCTCTACTAATAATTAATAATTA 164262
QY 2698 GCGGCGATGTGGCGAGGTGCTTTGATCCAGACTACTTGGAGGCTGAGGAGAGAT 2757
DB 164263 GCTGGCGGTGTGGCGAGGCTCTGATATCCAGCTACTCAAGAGGCTGAGGAGAGAT 164322
QY 2758 CACTTGAACCAAGAGGAGGCTGCACTGAGCTGAGATTGTGCCACTGCACTCCAGCC 2817
DB 164323 CACTTGAACCTGAGAGGCAAGGCTGCACTGAGCTGAGATTGTGCCACTGCACTCCAGCC 164382
QY 2818 TGGCAACCAAGAGCAAACTCTGCTGGAGAAAAAATTAATTAATTAATTAATTAATTAAT 2853
DB 164383 TGGCAATATAGAGCAAACTCTGCTGGAGAAAAAATTAATTAATTAATTAATTAATTAAT 164418

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RESULT 11
US-09-949-016-13615/c
; Sequence 13615, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 13615
; LENGTH: 13478
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(13478)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13615

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Query Match      8.7%; Score 248; DB 3; Length 13478;
Best Local Similarity 86.6%; Pred. No. 7.9e-56;

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: Sequence 11754, Application US/09949016
: Patent No. 6812339
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: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CL001307
: CURRENT APPLICATION NUMBER: US/09/949,016
: PRIOR FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 11754
: LENGTH: 75394
: TYPE: DNA
: ORGANISM: Human
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (1)...(75394)
: OTHER INFORMATION: n = A,T,C or G
:
: US-09-949-016-11754

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Query Match	8.64	Score 247	DB 3	Length 75394
Best Local Similarity	86.64	Pred. No. 2.1e-55		
Matches 271, Conservative	1	Mismatches 41	Indels 0	Gaps 0

Qy	2547	AAATAAATCATTAAGCGCAGAGCGTGGTGCATGCTGTATATCCACACATTGGTGG	2606
Db	68328	AATATAGTAAAAAATAGCCAGCGGGTGGTGTCTCAGGCTGTATATCCACGAATTTAGAG	68387
Qy	2607	GCTGAGGTGTGGATTAACCTGAGGTCAAGAGTTTCAGATTCAGGCTGGCCATATGCTGA	2666
Db	68388	GCTGAGGTGTGGATTAACCTGAGGTCAAGAGTTTCAGATTCAGGCTGGCCAAATGTGTA	68447
Qy	2667	AACCGTCTCTACTAATAATTAACAAAAATTAGCCGGCCATGTGTGGCAGGTGCTTGTATTC	2726
Db	68448	AAOCCCATCTCTACTAATAATTAACAAAAATTAGCCGGCCATGTGTGGCAGGTGCTTGTATTC	68507
Qy	2727	CCAGCTACTTGGAGAGCTGAGGCGAGAGAAATCACTTGAATCAGAGAGCGAGAGGTTGGAC	2786
Db	68508	CCAGCTACTTGGAGAGCTGAGGCGAGAGAAATCACTTGAATCAGAGAGCGAGAGGTTGGAC	68567
Qy	2787	TGAGCTGAGATTGTGCACATGCACCTCCAGCGCTGGGACACAAAGACAAAACTGTCTGGA	2846
Db	68568	TGAGCGAGATTTGTGCCATTTGCACCTCCAGCGCTGGGACACAAAGTGAATCTGTCTCAA	68627
Qy	2847	AAAAAAAAAAAAA	2859
Db	68628	AAAAAAAAAAGA	68640

RESULT 14  
US-09-750-580-1/c  
; Sequence 1, Application US/09750580

; Patent No. 6455280  
; GENERAL INFORMATION:

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; APPLICANT: Yen, Frances
; APPLICANT: Denison, Blake
; APPLICANT:

```

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; APPLICANT:  Bour, Barbara
; APPLICANT:  Bihahn, Bernard
; APPLICANT:  Bihahn, Bernard

```

; APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste

;  
; APPLICANT: Bougueleret, Lydie  
; APPLICANT: Ebbets-Reed, Dana

APPLICANT: Salter-Cid, Luisa  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH

FILE REFERENCE: 89.US2.CIP  
CURRENT APPLICATION NUMBER: US/09/750,580

1	CURRENT FILING DATE:	2000-12-28
2	PRIOR APPLICATION NUMBER:	US 09/599,362
3	PRIOR FILING DATE:	2000-06-21
4	PRIOR APPLICATION NUMBER:	PCT/IB00/0101
5	PRIOR FILING DATE:	2000-06-21
6	PRIOR APPLICATION NUMBER:	PCT/IB99/02058
7	PRIOR FILING DATE:	1999-12-20
8	PRIOR APPLICATION NUMBER:	US 49/469/099
9	PRIOR FILING DATE:	1999-12-21
10	PRIOR APPLICATION NUMBER:	US 60/113,686
11	PRIOR FILING DATE:	1998-12-22
12	PRIOR APPLICATION NUMBER:	US 60/141,032
13	PRIOR FILING DATE:	1999-06-25
14	NUMBER OF SEQ. ID NOS:	6
15	SOFTWARE:	Patent.pm
16	SEQ ID NO 1	
17	LENGTH:	81001
18	TYPE:	DNA
19	ORGANISM:	Homo sapiens
20	FEATURE:	
21	NAME/KEY:	misc_feature
22	LOCATION:	10946..12946
23	OTHER INFORMATION:	5'regulatory region
24	NAME/KEY:	exon
25	LOCATION:	12947..12958
26	OTHER INFORMATION:	exon 1
27	NAME/KEY:	exon
28	LOCATION:	13470..13526
29	OTHER INFORMATION:	exon 2
30	NAME/KEY:	exon
31	LOCATION:	13641..13752
32	OTHER INFORMATION:	exon 3
33	NAME/KEY:	exon
34	LOCATION:	14271..15968
35	OTHER INFORMATION:	exon 4
36	NAME/KEY:	misc_feature
37	LOCATION:	15969..17969
38	OTHER INFORMATION:	3'regulatory region
39	NAME/KEY:	allele
40	LOCATION:	1239
41	OTHER INFORMATION:	20-828-311 : polymorphic base C or T
42	NAME/KEY:	allele
43	LOCATION:	12347
44	OTHER INFORMATION:	17-42-319 : polymorphic base C or T
45	NAME/KEY:	allele
46	LOCATION:	15241
47	OTHER INFORMATION:	17-41-250 : polymorphic base C or T
48	NAME/KEY:	allele
49	LOCATION:	42218
50	OTHER INFORMATION:	20-841-149 : polymorphic base A or G
51	NAME/KEY:	allele
52	LOCATION:	45442
53	OTHER INFORMATION:	20-842-115 : polymorphic base A or G
54	NAME/KEY:	allele
55	LOCATION:	77058
56	OTHER INFORMATION:	20-853-415 : polymorphic base C or T
57	NAME/KEY:	primer_bind
58	LOCATION:	929..949
59	OTHER INFORMATION:	20-828-pu
60	NAME/KEY:	primer_bind
61	LOCATION:	1357..1377
62	OTHER INFORMATION:	20-828-1p complement
63	NAME/KEY:	primer_bind
64	LOCATION:	12029..12050
65	OTHER INFORMATION:	17-42-pu
66	NAME/KEY:	primer_bind
67	LOCATION:	12581..12603
68	OTHER INFORMATION:	17-42-1p complement
69	NAME/KEY:	primer_bind
70	LOCATION:	14992..15012
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73	LOCATION:	15460..15482

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OTHER INFORMATION: 17-41.tp complement
NAME/KEY: primer bind
LOCATION: 42070..42090
OTHER INFORMATION: 20-841.pu
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LOCATION: 42572..42591
OTHER INFORMATION: 20-841.tp complement
NAME/KEY: primer bind
LOCATION: 45328..45347
OTHER INFORMATION: 20-842.pu
NAME/KEY: primer bind
LOCATION: 45863..45883
OTHER INFORMATION: 20-842.tp complement
NAME/KEY: primer bind
LOCATION: 76644..76664
OTHER INFORMATION: 20-853.pu
NAME/KEY: primer bind
LOCATION: 77166..77185
OTHER INFORMATION: 20-853.tp complement
NAME/KEY: primer bind
LOCATION: 1230..1238
OTHER INFORMATION: 20-828-311.mis
NAME/KEY: primer bind
LOCATION: 1240..1258
OTHER INFORMATION: 20-828-311.mis complement
NAME/KEY: primer bind
LOCATION: 12328..12346
OTHER INFORMATION: 17-42-319.mis
NAME/KEY: primer bind
LOCATION: 12348..12366
OTHER INFORMATION: 17-42-319.mis complement
NAME/KEY: primer bind
LOCATION: 15222..15240
OTHER INFORMATION: 17-41-250.mis
NAME/KEY: primer bind
LOCATION: 15242..15260
OTHER INFORMATION: 17-41-250.mis complement
NAME/KEY: primer bind
LOCATION: 42199..42217
OTHER INFORMATION: 20-841-149.mis
NAME/KEY: primer bind
LOCATION: 42219..42237
OTHER INFORMATION: 20-842-115.mis
NAME/KEY: primer bind
LOCATION: 45423..45441
OTHER INFORMATION: 20-842-115.mis complement
NAME/KEY: primer bind
LOCATION: 45443..45461
OTHER INFORMATION: 20-842-115.mis complement
NAME/KEY: primer bind
LOCATION: 77039..77057
OTHER INFORMATION: 20-853-415.mis
NAME/KEY: primer bind
LOCATION: 77059..77077
OTHER INFORMATION: 20-853-415.mis complement
NAME/KEY: primer bind
LOCATION: 1227..1251
OTHER INFORMATION: 20-828-311.probe
NAME/KEY: primer bind
LOCATION: 12335..12359
OTHER INFORMATION: 17-42-319.probe
NAME/KEY: primer bind
LOCATION: 15229..15253
OTHER INFORMATION: 17-41-250.probe
NAME/KEY: primer bind
LOCATION: 42206..42230
OTHER INFORMATION: 20-841-149.probe
NAME/KEY: primer bind
LOCATION: 45430..45454
OTHER INFORMATION: 20-842-115.probe
NAME/KEY: primer bind
LOCATION: 77046..77070
OTHER INFORMATION: 20-853-415.probe

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US-09-750-580-1
Query Match      8.6%; Score 247; DB 3; Length 81001;
Best Local Similarity 86.6%; Pred. No. 2, 2e-55;
Matches 271; Conservative 1; Mismatches 41; Indels 0; Gaps 0;

QY 2547 AAAATGAAATCATTTAGGCGGAGGCGTGTGCTCATCTTTGTAATCCAGACATTTGGTAG 2606
DB 65051 ATAGAGAAATGTGTGTGCGGAGGTCAGTGGCTCAGCGCTGTATATCCAGACATTTGGAG 64992
QY 2607 GCTGAGTGTGTGTGATCACTGAGGTCAGAGTTGCAATCCAGCTGGGCCAATATGCTGA 2666
DB 64991 GCCAAGTGTGTGTGATCACTGAGGTCAGAGTTGCAATCCAGCTGGGCCAATATGCTGA 64932
QY 2667 AACCTGTCTCTAATAAATTAAGCGGCAATGTGGGAGGTCCTGTATC 2726
DB 64931 AACCCGCTCTATTAATAAATTAAGCGGCAATGTGGGAGGTCCTGTATC 64872
QY 2727 CCAGCTACTTGGAGGCTGAGGAGGAGATCACTTGAACCAAGAAAGGAGGTTGCAC 2786
DB 64871 CCAGCTACTGAGGCTGAGGAGGAGATCACTTGAACCGGAGGAGGTTGCAG 64812
QY 2787 TGAGCTGAGTGTGCACTGCACTCCAGCTTGGGCAAGAGCAAACTGTCTGGA 2846
DB 64811 TGAGCTGAGTGTGCACTGCACTCCAGCTTGGGCAAGAGCAAACTGTCTGGA 64752
QY 2847 AAAAAAAAAAAAAA 2859
DB 64751 AAAAAAAAAAAAAA 64739

RESULT 15
US-09-949-016-186635/C
; Sequence 186635, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 186635
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-186635

Query Match      8.6%; Score 246.6; DB 3; Length 601;
Best Local Similarity 81.7%; Pred. No. 2, 9e-56;
Matches 282; Conservative 2; Mismatches 61; Indels 0; Gaps 0;

QY 2513 CTGCTGTAATAAATTAATGCTGAATAATTTCTTAATAATGAAATCAATAGGCGGAGGCTG 2572
DB 369 CTGAGCTACCACTTACCAAACTTACTATATGACTTAAGAAATGTTGCGGCGGCTG 310
QY 2573 GTGGCTCAGCTTGTATATCCAGCACTTGTGTGAGTGTGAGTGTGATCACTTGAAGT 2632
DB 309 GTGGCTCAGCTTGTATATCCAGCACTTGTGTGAGTGTGAGTGTGATCACTTGAAGT 250
QY 2633 CAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 2692
DB 249 CAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 190
QY 2693 AATTAGCCGCGCATGTGTGCGAGGTGCTTGTATCCAGCTACTTGTGAGGCTGAGCGAG 2752

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Db	189	AATTAGCCAGGCAATGGTGCCACCTGCTGTAAATCCAGCTACTTGGAGGCTGAGGCAGG	130
Qy	2753	AGATCACTTGAACCAAGGAAGCAGAGGTTGCACTGAGCTGAGATTGTGCCACTGCACTC	2812
Db	129	AGATCACTTGAACCTGGAGGCAAGAGTTGCAGTGAGCCGAGATGCGCACCACTGCACTC	70
Qy	2813	CAGCTGGGCAACAGAGCAAACTCTGTCTGAAAAA	2857
Db	69	CAGCTGGGCAACAGAGCAAACTCTCAAAAAA	25

Search completed: October 14, 2006, 17:27:56  
 Job time : 521 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus.p2n model

Run on: October 14, 2006, 14:40:43 ; Search time 1964 Seconds

(without alignments)  
5902.945 Million cell updates/sec

Title: US-10-667-289-2

Perfect score: 3326

Sequence: 1 MNXVTIQMNAVILYILFSW.....TYPQNLBSHFNRISLLEK 629

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Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

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Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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-Q=/abs/ABSSWEB.spool/US1067289/runat.13102006.111541.24520/app\_query.fasta.1  
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-USRR=US1067289.OCEN.1.1.675.0runat.13102006.111541.24520 -NCFU=6 -ICPU=3  
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-MAIN TIMEOUT=30 -THEADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications NA.Main:

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3324	99.9	2859	3	US-09-853-180-1
					Sequence 1, Appl1

2	3324	99.9	2859	9	US-10-797-157-5	Sequence 5, Appl1
3	3324	99.9	2859	9	US-10-720-026-1	Sequence 1, Appl1
4	3324	99.9	2859	10	US-10-667-289-1	Sequence 1, Appl1
5	3324	99.9	2859	10	US-10-667-290-1	Sequence 1, Appl1
6	3314	99.6	1890	3	US-09-972-708-20	Sequence 20, Appl1
7	3314	99.6	1890	8	US-10-715-667-20	Sequence 9, Appl1
8	3314	99.6	1890	6	US-10-105-930-9	Sequence 19, Appl1
9	3314	99.6	2830	6	US-09-972-708-19	Sequence 19, Appl1
10	3314	99.6	2830	8	US-10-715-667-19	Sequence 19, Appl1
11	3292	99.0	2123	6	US-10-105-930-5	Sequence 5, Appl1
12	2952	88.8	1638	3	US-09-972-708-22	Sequence 22, Appl1
13	2952	88.8	1638	8	US-10-715-667-22	Sequence 22, Appl1
14	2280.5	68.6	1935	8	US-09-972-708-29	Sequence 29, Appl1
15	2280.5	68.6	1935	8	US-10-715-667-29	Sequence 29, Appl1
16	2192	65.9	1301	6	US-10-105-930-7	Sequence 7, Appl1
17	2175	65.4	1479	6	US-10-105-930-3	Sequence 3, Appl1
18	2039	61.3	1155	6	US-10-247-463-1	Sequence 1, Appl1
19	2039	61.3	1155	13	US-11-016-106-1	Sequence 1, Appl1
20	1868	56.2	1071	3	US-09-972-708-24	Sequence 24, Appl1
21	1868	56.2	1071	8	US-10-715-667-24	Sequence 24, Appl1
22	1747	52.5	1152	6	US-10-247-463-3	Sequence 3, Appl1
23	1747	52.5	1152	13	US-11-016-106-3	Sequence 3, Appl1
24	1695	51.0	1784	6	US-10-105-930-1	Sequence 1, Appl1
25	335	10.1	637	6	US-10-027-632-210413	Sequence 210413,
26	335	10.1	637	7	US-10-027-632-210413	Sequence 210413,
27	286	8.6	360	6	US-10-105-930-23	Sequence 23, Appl1
28	268	8.1	1293	10	US-10-750-185-59162	Sequence 59162, A
29	268	8.1	1293	10	US-10-750-623-59162	Sequence 59162, A
30	256.5	7.7	2995	7	US-10-425-529-17	Sequence 17, Appl1
31	256.5	7.7	2995	9	US-10-645-012-17	Sequence 17, Appl1
32	250	7.5	412	3	US-09-864-761-16612	Sequence 16612, A
33	225.5	6.8	3274	16	US-11-136-527-2009	Sequence 2009, Ap
34	221	6.6	4023	9	US-10-398-666-11	Sequence 11, Appl1
35	216	6.5	4040	10	US-10-370-7158-67	Sequence 67, Appl1
36	216	6.5	4040	10	US-10-929-182-19	Sequence 19, Appl1
37	210	6.3	2838	10	US-10-450-763-12224	Sequence 12224, A
38	209	6.3	3085	3	US-09-829-4728-8	Sequence 8, Appl1
39	209	6.3	3085	7	US-10-177-293-229	Sequence 229, App
40	209	6.3	3085	7	US-10-172-118-736	Sequence 736, App
41	209	6.3	3085	7	US-10-295-027-73	Sequence 73, Appl1
42	209	6.3	3085	8	US-10-058-8704-31	Sequence 31, Appl1
43	209	6.3	3085	8	US-10-342-887-736	Sequence 736, App
44	209	6.3	3085	8	US-10-641-643-1131	Sequence 1131, Ap
45	209	6.3	3358	6	US-10-116-802-208	Sequence 208, App

#### ALIGNMENTS

RESULT 1  
US-09-853-180-1  
Sequence 1, Application US/09853180  
Publication No. US20030017617A1  
GENERAL INFORMATION:  
APPLICANT: Chirica, Madeline  
APPLICANT: Parham, Christi L.  
APPLICANT: Kastelein, Robert A.  
APPLICANT: Moore, Kevin W.  
TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods.  
FILE REFERENCE: DX01074  
CURRENT APPLICATION NUMBER: US/09/853,180  
CURRENT FILING DATE: 2001-05-10  
PRIORITY APPLICATION NUMBER: 60/203,426  
PRIORITY FILING DATE: 2000-05-10  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 2859  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (119)..(2005)  
OTHER INFORMATION:

US-09-853-180-1

## Alignment Scores:

Pred. No.:	0	Length:	2859
Score:	3324.00	Matches:	629
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	99.9%	Indels:	0
DB:	3	Gaps:	0

US-10-667-289-2 (1-629) x US-09-853-180-1 (1-2859)

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## RESULT 2

US-10-797-157-5

; Sequence 5, Application US/10797157

; Publication No. US20040223969A1

; GENERAL INFORMATION:

; APPLICANT: Ofc. Martin



APPLICANT: McClanahan, Terrill K.  
TITLE OF INVENTION: USES OF IL-23 AGONISTS AND ANTAGONISTS; RELATED REAGENTS  
FILE REFERENCE: D06022US01  
CURRENT APPLICATION NUMBER: US/10/797,157  
CURRENT FILING DATE: 2004-03-09  
PRIORITY FILING DATE: 2003-03-10  
PRIORITY FILING DATE: 2003-03-10  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 5  
LENGTH: 2859  
TYPE: DNA  
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LOCATION: (119)..(2005)  
FEATURE:  
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LOCATION: (188)..(2005)  
US-10-797-157-5

Alignment Scores:  
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Score: 3324.00 Matches: 629  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 99.9% Indels: 0  
DB: 9 Gaps: 0

US-10-667-289-2 (1-629) x US-10-797-157-5 (1-2859)

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RESULT 3  
US-10-720-026-1  
; Sequence 1, Application US/10720026  
; Publication No. US20040258686A1  
; GENERAL INFORMATION:  
; APPLICANT: Chirica, Madeline  
; APPLICANT: Parham, Christi L.  
; APPLICANT: Kastelein, Robert A.  
; APPLICANT: Moore, Kevin W.  
; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods.  
; FILE REFERENCE: DX0107481K  
; CURRENT APPLICATION NUMBER: US/10/720,026  
; CURRENT FILING DATE: 2003-11-21  
; PRIOR APPLICATION NUMBER: 60/203,426  
; PRIOR FILING DATE: 2000-05-10  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
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; ORGANISM: Homo sapiens  
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; LOCATION: (119)..(2005)  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: (188)..(2005)  
US-10-720-026-1  
Alignment Scores:  
Pred. No. 0 Length: 2859  
Score: 3324.00 Matches: 629  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 99.9% Indels: 0  
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US-10-667-289-2 (1-629) x US-10-720-026-1 (1-2859)  
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Qy      401 ProAsnMetLysAsnSerAsnValValLysMetLeuGlnLubAsnSerGlyLeuMetAsn
Db      1319 CTTATATGAAAAACACCATGTTGTGAAAATGCTACAGAAAATGTAACCTTATGTAAT
Qy      421 AsnAsnSerSerGlyGlnValLeuTyrValAspProMetIleThrGlyIleGlyIle
Db      1379 AATATATCCAGTGCAGTCTCTATATGTTGATCCCATGATTCAGAGATTAAGAAATC
Qy      441 PheIleProGlyHisGlySerProThrAspTyrLysLeuGlnLubAsnThrGlyProLeuGlnThr
Db      1439 TTCTATCCAGAACACAAAGCTTACAGACTTACAGAGAGAAATACAGAGACCCCTGGAGACA
Qy      461 ArgAspTyrProGlnAsnSerLeuPheAspAsnThrThrValValTyrIleProAspLeu
Db      1499 AGAGACTACCCGCAAACTCGCTATTCGACATATCTACATGTTATATATTCCTGATCTC
Qy      481 AsnThrGlyTyrLysProGlnIleSerAsnPheLeuProGlyLysSerHisLeuSerAsn
Db      1559 AACCTGATATTAACCCCAATTTCAATTTCTGCTGAGGAAACCACTTCACGCAAT
Qy      501 AsnAsnGlnIleThrSerLeuThrLeuLysProProValAspSerLeuAspSerGlyAsn
Db      1619 AATATATTAATATCTTCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT
Qy      521 AsnProArgLeuGlnLysHisProAsnPheAlaPheSerValSerSerValAsnSerLeu
Db      1679 AATCCCAAGTTACAAAGCATTCCTAATTTGCTTTCTGTTCAAGTGAATTCATCTA
Qy      541 SerAsnThrIlePheLeuGlyGlnLeuSerLeuIleLeuAsnGlnGlyLysSerSer
Db      1739 AGCAACACAAATATTTCTTGAAGATTAAGCTCATATTAATCAAGAGAAATGCAATCTC
Qy      561 ProAspIleGlnAsnSerValGlnGlnGlnThrThrMetLeuGlnLubAsnAspSerPro
Db      1799 CCTGACATTAACAACTAGTAGAGAGAGAAACCACTGCTTTGAGAAATGATTCACCC
Qy      581 SerGlnThrIleProGlnGlnThrLeuLeuProAspGlnPheValSerCysLeuGlyIle
Db      1859 AGTGAACATTAATCCAGAACAGACCCCTGCTTCTGATGAATTTGTCTCTGTTTGGGATC
Qy      601 ValAsnGlnGlnLeuProSerIleAsnThrTyrPheProGlnAsnIleLeuGlnSerHis
Db      1919 GTGATATAGAGAGTTGCCATCATTAATATTAATTTTCCACAAATATTTGGAAGCCAC
Qy      621 PheAsnArgIleSerLeuLeuGlnLys 629
Db      1979 TTCAATAGAGATTCACTTGGAAAG 2005

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RESULT 5
US-10-667-290-1
; Sequence 1, Application US/10667290
; Publication No. US20050100918A1
; GENERAL INFORMATION:
; APPLICANT: Chirica, Madeline

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; APPLICANT: Parham, Christl L.
; APPLICANT: Kastelejn, Robert A.
; APPLICANT: Moore, Kevin W.
; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods.
; FILE REFERENCE: DX01074
; CURRENT APPLICATION NUMBER: US/10/667,290
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/853,180B
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,426
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 2859
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (119)..(2005)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (127)..(127)
; OTHER INFORMATION: k means g or t/u. See page 12, line 34, of patent application as
; OTHER INFORMATION: originally filed.
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (188)..(2005)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (563)..(563)
; OTHER INFORMATION: x means g or a. See page 12, line 36, of patent application as
; OTHER INFORMATION: originally filed.
US-10-667-290-1

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Alignment Scores:
Pred. No.: 0 Length: 2859
Score: 3324.00 Matches: 629
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 99.9% Indels: 0
DB: Gaps: 0

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US-10-667-289-2 (1-629) x US-10-667-290-1 (1-2859)

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Qy      1 MetAsn**ValThrIleGlnTrpAspAlaValIleAlaLeuTyrIleLeuPheSerTrp 20
Db      119 ATGATCAKATCACTTCAATGAGATGCAATGATGATGATGATGATGATGATGATGATG
Qy      21 CysHisGlyGlyIleThrAsnIleAsnGlyHisIleIleTrpValGlnProIleThr 40
Db      179 TGCATGAGAGATTAACAAATATTAATGATGATGATGATGATGATGATGATGATGATG
Qy      41 IlePheIleMetGlyMetAsnIleSerIleTyrCysGlnAlaAlaIleLysAsnGln 60
Db      239 ATTTTAAGATGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
Qy      61 ProArgLysLeuHisPheTyrLysAsnGlyIleLysGlnLubArgPheGlnIleThrArgIle 80
Db      299 CGAAGGAACCTCAATTTTATTAATAATGCGATCAAGAAAGATTTCAATCAAGAGATT 358
Qy      81 AsnLysThrThrAlaArgLeuTrpTyrLysAsnPheLeuGlnLubProHisAlaSerMetTyr 100
Db      359 AATTAACAAACACACTGGCTTGTGTATTAATACTTTCTGGAACACATGCTTCTATGTAC 418
Qy      101 CysThrAlaGlyCysProLysHisPheGlnGlnThrLeuIleCysGlyLysAspIleSer 120
Db      419 TGCATGCTGAAATGCTCCAAACATTTTCAAGAACACTGATATGATGAGAAAGCAATTTCT 478
Qy      121 SerGlyTyrProProAspIleProAspGlnValThrCysValIleTyrGlyTyrSerGly 140
Db      479 TGTGATATCGCCAGATATTTCTGATGAGATTAACCTGTCTATTTATGAAATTTCAAGGC 538

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QY 141 AsnMetThrCysThrTrpAsnAla\*\*LysLeuThrTyrIleAspThrLysTyrValVal 160  
 DB 539 AATGATGCTGCACTGGAAATGCTGGAGAGCTCACTACATAGACAAATAATAGTGTGTA 598  
 QY 161 HisValLysSerLeuGluThrGluGluGluGlnGlnTyrLeuThrSerSerTyrIleAsn 180  
 DB 599 CATGTGAAGAGTTTGAAGACAGAGAGAGACAGATCTCACTCAAGCTAATATTAAC 658  
 QY 181 LLeSerThrAspSerLeuGlnGlyLysLeuTyrLeuValTTPValGlnAlaAlaAsn 200  
 DB 659 ATCTCCACTGATTCATTAACAAGTGGCAAGAGTACTTGTTGGGTCCAGACAGCAAC 718  
 QY 201 AlaLeuGlyMetGluGluSerLysGlnLeuGlnIleHisLeuAspAspIleValIlePro 220  
 DB 719 GCATAGGCACTGAGAGAGTCAAAACAATCACTCAATTCACCTGATGATATAGTATACCT 778  
 QY 221 SerAlaAlaValIleSerArgAlaGluThrIleAsnAlaThrValProLysThrIle 240  
 DB 779 TCTGACAGCCGTCATTTCCAGGGCTGAGACTATTAATCTACAGTCCCAAGACCATTAAT 838  
 QY 241 TyrTrpAspSerGlnThrThrIleGluLysValSerCysGluMetArgTyrLysAlaThr 260  
 DB 839 TATTGGATAGTCAAAACAACATTTGAAGAGTTCCTGTGAATGAGATACAAAGGCTTACA 898  
 QY 261 ThrAsnGlnThrTrpAsnValLysGluPheAspThrAspPheThrTyrValGlnGlnSer 280  
 DB 899 ACBAACCAAACTTGGAAATGTTAAAGATTTGACACCAATTTTACATATGTCACCACTCA 958  
 QY 281 GluPheTyrLeuGluProAsnIleLysTyrValPheGlnValArgCysGlnGluThrGly 300  
 DB 959 GAATTCACCTTGGAGCCAAACATTAAGTACGTATTTCAAGTGAATGTCAAGAAACAGGC 1018  
 QY 301 LysArgTyrTrpGlnProTyrPheSerProPhePheHisTyrThrProGluThrValPro 320  
 DB 1019 AAAAGGTACTGGCAGCCCTTGAAGTCCCTTTTTCATTAACACCTGAAACAGTTCCTCC 1078  
 QY 321 GlnValThrSerLysAlaPheGlnHisAspThrTrpAsnSerGlyLeuThrValAlaSer 340  
 DB 1079 CAGCTCATCATTAAGATTCCTCAACATGACATGAAATCTGGGCTTACACGTTGCTTCC 1138  
 QY 341 LLeSerThrGlyHisLeuThrSerAspAsnArgLysAspIleGlyLeuLeuLeuMet 360  
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 QY 361 IleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAlaArgSerPhe 380  
 DB 1199 ATGCTCTTGGCTGTATGATGTTCAATCTTCTTGTGATGGGATATTAAACAGATCAATTC 1258  
 QY 381 ArgThrGlyIleLysArgArgIleLeuLeuLeuIleProLysTrpLeuTyrGluAspIle 400  
 DB 1259 CGAATCTGGATTTAAAGAGAGATCTTATTTGTTAATACCAAGTGGCTTTATGAGATATTT 1318  
 QY 401 ProAsnMetLysAsnSerAsnValValLysMetLeuGlnLysAsnSerGluLeuMetAsn 420  
 DB 1319 CTTAATATGAAAAACAGCATGTTGTGAATAATGCTACAGAAAAATAGTGAATCTTATGAAAT 1378  
 QY 421 AsnAsnSerSerGluGlnValLeuTyrValAspProMetIleThrGluIleLysGluIle 440  
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 DB 1439 TTCAATCCAGAAACAAGCTTACAGACTTACAAAGAGAGATACAGAACCCCTGGAGACA 1498  
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 QY 501 AsnAsnGluIleThrSerLeuThrLeuLysProProValAspSerLeuAspSerGlyAsn 520

DB 1619 AATATGAAATTAATCTTCTTAACCTTAACCAACCACTGATTCCTTGACTCAGAAAT 1678  
 QY 521 AsnProArgLeuGlnLysHisProAsnPheAlaPheSerValSerSerValAsnSerLeu 540  
 DB 1679 AATCCAGGTGTACAAAAGCATCTTAATTTGCTTTTCTGTTCACAGTGAATTCCTA 1738  
 QY 541 SerAsnThrIlePheLeuGlyGluLeuSerLeuIleLeuAsnGlnGlyGluCysSerSer 560  
 DB 1739 AGCAACCAATATTTCTTGGAGATTTAAGCTCATATTAATCAAGAGATGCAATTCCT 1798  
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 DB 1799 CTGACATTAACAACCTCAGTAGAGAGAGAACCAACCATGCTTTTGAATAATGATTCACCC 1858  
 QY 581 SerGluThrIleProGluGlnThrLeuLeuProAspGluPheValSerCysLeuGlyIle 600  
 DB 1859 AGTGAACATATTCAGAACAGACCCCTGCTTCGATGAATTTGCTCTGTTGGGAGATC 1918  
 QY 601 ValAsnGluGluLeuProSerIleAsnThrTyrPheProGluAsnIleLeuGluSerHis 620  
 DB 1919 GTGAAATGAGAGTGGCCATCTTATTAATCTTATTTTCCAAATAATTTTGGAAAGCCAC 1978  
 QY 621 PheAsnArgIleSerLeuLeuGlyLys 629  
 DB 1979 TTCAATAGATTTCACTCTTGAAGAAAG 2005  
 RESULT 6  
 US-09-972-708-20  
 ; Sequence 20, Application US/09972708  
 ; Publication No. US20030059871A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Immunex Corporation  
 ; APPLICANT: Cosman, David J.  
 ; APPLICANT: Mosley, Bruce A.  
 ; APPLICANT: Bird, Timothy A.  
 ; APPLICANT: Dubose, Robert F.  
 ; APPLICANT: Wiley, Steven R.  
 ; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPRI2  
 ; FILE REFERENCE: 3160-B  
 ; CURRENT APPLICATION NUMBER: US/09/972,708  
 ; CURRENT FILING DATE: 2001-10-05  
 ; NUMBER OF SEQ ID NOS: 29  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 20  
 ; LENGTH: 1890  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-972-708-20  
 Alignment Scores:  
 Pred. No.: 0 Length: 1890  
 Score: 3314.00 Matches: 626  
 Percent Similarity: 99.5% Conservative: 0  
 Best Local Similarity: 99.5% Mismatches: 3  
 Query Match: 99.6% Indels: 0  
 Gaps: 0  
 US-10-667-289-2 (1-629) x US-09-972-708-20 (1-1890)  
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 DB 61 TGTCAATGAGAGATTTCAAAATATAAATGCTGCTGACACATCTGCGGTAGAACAGACACA 120  
 QY 41 IlePheLysMetGlyMetAsnIleSerIleTyrCysGlnAlaAlaIleLysAsnCysGln 60  
 DB 121 ATTTTAAGATGGATTAATCTTAATATTTGTCACAGACACAAATTAAGAACTGGCAA 180  
 QY 61 ProArgLysLeuHisPheTyrLysAsnGlyIleLysGluLysArgPheGlnIleThrArgIle 80

181 CCAAGGAACTTCATTTTATTAATAAAGCATCAAAAGATTTCACAAAGATT 240  
 81 AsnLysThrThrAlaArgLeuTrpTyrLysAsnPhelLeuGluProHisAlaSerMetTyr 100  
 241 AATAAAACAACAGCTCCGCTTTGGTATTAATAAATTTCTGAAACCAATGCTCTTATATAC 300  
 101 CysThrAlaGluCysProLysHisPheGlnGluThrLeuIleCysGlyLysAspIleSer 120  
 301 TGCACTGCTGAAATGTCCTCAAAATTTTCAAGAGACACATGATATGTGAAAAAGACATTTCT 360  
 121 SerGlyTyrProProAspIleProAspGluValThrCysValIleIleTyrGlyTyrSerGly 140  
 361 TCGGATATCCGCGCAAGATATTCCTGATGAAGTAACTGTGCTCATTTATGAAATATTCAGGC 420  
 141 AsnMetThrCysThrTPAsnAla\*\*LysLeuThrTyrIleAspThrLysTyrValVal 160  
 421 AACATGACTTGCACTGGAATGCTGGAGAGCTCACCTACATACCAAAATACGTGTGTA 480  
 161 HisValLysSerLeuGluThrGluGluGluGlnGlnIleThrLeuThrSerSerTyrIleAsn 180  
 481 CATGTGAAGAGTTTAAAGACAGAAAGAAAGCAAGATATCTCACCTCAAGCTATATTATAC 540  
 181 IleSerThrAspSerLeuGlnGlyLysLysTyrLeuValTyrValGlnAlaAlaAsn 200  
 541 ATCCCACTGATTCATTACAAAGGTGCAAGAGTACTGTGGTTCAGCAAGCAAGCAAC 600  
 201 AlaleuGlyMetGluGluSerLysGlnLeuGlnIleHisLeuAspAspIleValIlePro 220  
 601 GCATCAGCCTGAGAGAGTCAAAACCACTGCATTCCTGAGATGATATGATATCT 660  
 221 SerAlaIleValIleSerArgAlaGluThrIleAsnAlaThrValProLysThrIleIle 240  
 661 TCTGCAACCCGCTCATTTCCAGGGCTGAGACTATAATCTACAGGCCCAAGACCATATTT 720  
 241 TyrTrpAspSerGlnThrThrIleGluLysValSerCysGluMetAlaGlyTyrValAlaThr 260  
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 261 ThrAsnGlnThrTPAsnValLysGluPheAspThrAsnPhetTyrValGlnGluSer 280  
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 281 GluPheTyrLeuGluProAsnIleLysTyrValPheGlnValArgCysGlnGluThrGly 300  
 841 GAATTTCTACTTGAGCCAAACATTAAGTACGTAATTCAGAGGATGCAAGAAACAGGC 900  
 301 LysArgTyrTrpGlnProTyrPheSerProPhePheHisLysThrProGluThrValPro 320  
 901 AAAAGGTACTGGCAGCCCTTGAGTTCCTGTTTTCATTAACCACTGAAACAGTCC 960  
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 1201 CCTATATGAAAAACAGCAATGTTGTGAATATGCTACAGAAATATGGAATATGAT 1260  
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 481 AsnThrGlyTyrLysProGluIleSerAsnPheLeuProGluLysSerHisLeuSerAsn 500  
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 501 AsnAsnGluIleThrSerLeuThrLeuLysProProValAspSerLeuAspSerGlyAsn 520  
 1501 AATATGAAATTTACTTCTTAAACCTTAAACCAAGTATTCCTTAGACTCAGGAAAT 1560  
 521 AsnProArgLeuGlnLysHisProAsnPheAlaPheSerValSerSerValAsnSerLeu 540  
 1561 AATCCCAAGTTTACAAAGCATCTTAATTTGCTTTTCTGTTCAAGTGTGAATTCCTA 1620  
 541 SerAsnThrIlePheLeuGluGluLysSerLeuIleLeuAsnGlnGluGlyCysSerSer 560  
 1621 AGCAACCAATATTTCTTGGAGATTAAGCTCATATTAATCAAGAGAAATGCAATTTCT 1680  
 561 ProAspIleGlnAsnSerValGluGluGluThrThrMetLeuLeuGluAsnAspSerPro 580  
 1681 CTGACATTAACAAATCTAGTAAAGAGAGAAACCAACCATGCTTTTGGAAAAATGATTCACC 1740  
 581 SerGluThrIleProGluGlnThrLeuLeuProAspGluPheValSerCysLeuGlyIle 600  
 1741 AGTGAACCTATTCAGAAACAGACCCTGCTTCTGATGAATTTTCTCTGTTGGGGATC 1800  
 601 ValAsnGluGluLeuProSerIleAsnThrTyrPheProGluAsnIleLeuGluSerHis 620  
 1801 GTGAATGAGAGTGGCCATCTATTAATCTTATTTTCCAAATATTTTGGAAAGCCAC 1860  
 621 PheAsnArgIleSerLeuLeuGluLys 629  
 1861 TTCAATAGATTTTCACTTGGAAAG 1887

RESULT 7  
 US-10-715-667-20  
 ; Sequence 20, Application US/10715667  
 ; Publication No. US20040152161A1  
 GENERAL INFORMATION:  
 ; APPLICANT: Immunex Corporation  
 ; APPLICANT: Coeman, David J.  
 ; APPLICANT: Mosley, Bruce A.  
 ; APPLICANT: Bird, Timothy A.  
 ; APPLICANT: Dubose, Robert F.  
 ; APPLICANT: Wiley, Steven R.  
 TITLE OR INVENTION: HEMATOPOIETIN RECEPTORS HPR1 AND HPR2  
 FILE REFERENCE: 3160-B  
 ; CURRENT APPLICATION NUMBER: US/10/715,667  
 ; CURRENT FILING DATE: 2003-11-14  
 ; PRIOR APPLICATION NUMBER: US/09/972,708  
 ; PRIOR FILING DATE: 2001-10-05  
 ; NUMBER OF SEQ ID NOS: 29  
 ; SOFTWARE: Patentin version 3.1  
 ; SEQ ID NO 20  
 ; LENGTH: 1890  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-715-667-20

Alignment Scores:  
 Pred. No.: 0  
 Score: 3314.00  
 Percent Similarity: 99.5%  
 Best Local Similarity: 99.5%  
 Query Match: 99.6%

Length: 1890  
 Matches: 626  
 Conservative: 0  
 Mismatches: 3  
 Indels: 0



DB: 8 Caps: 0  
US-10-667-289-2 (1-629) x US-10-715-667-20 (1-1890)  
QY 1 MetAsn\*\*\*ValThrIleGlnTPAspAlaValIleAlaLeuTyrIleLeuPheSerTrp 20  
DB 1 ATGAATCAGGTCACTATTCAATGGAGATGACAGTAATAGCCCTTAAACATACATCTTCAGCTGG 60  
QY 21 CyHHisGlyGlyIleThrAsnIleAsnCySerGlyHisIleTrpValGluProAlaThr 40  
DB 61 TGTCAATGAGAAATTAACAATATAAATGCTGCGCAACATCTGGAGAACCAAGCCACA 120  
QY 41 IlePheLeuMetGlyMetAsnIleSerIleTyrCysGlnAlaAlaIleLeuAsnCySerGln 60  
DB 121 ATTTTAAAGTGGATGAAATCTCTATATATTGCCAACACAGATTAAGAATGCCAA 180  
QY 61 ProArgLeuLeuHisPheTyrLeuAsnGlyIleLeuGluArgPheGlnIleThrArgIle 80  
DB 181 CCAAGGAACTTCATTTTATAAAATGCGATCAAGAAAGATTCAATCAACAAGGATT 240  
QY 81 AsnLeuThrThrAlaArgLeuTyrTyrLeuAsnPheLeuGluProHisAlaSerMetTyr 100  
DB 241 AATMAAACACACACTCGCTTGGTATMAAACTTCTTGGAACCACTGCTTATGTATC 300  
QY 101 CysThrAlaGluCysProLeuHisPheGlnGluThrLeuIleCysGlyLeuAspIleSer 120  
DB 301 TGCATCTGCTAAATGCTCCCAACATTTTCAAGACACTGATATGTGAAAAGACATTTCT 360  
QY 121 SerGlyTyrProProAspIleProAspGluValThrCysValIleTyrGluTyrSerGly 140  
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QY 141 AsnMetThrCysThrTrpAsnAla\*\*\*LeuLeuThrTyrIleAspThrIleTyrValVal 160  
DB 421 AATCATGCTTGCACTGGAATGCTGGAGACCTCACTCAATAGACACAAATATCTGTGTA 480  
QY 161 HisValIleSerLeuGluThrGluGluGlnGluIleThrLeuPheThrSerTyrIleAsn 180  
DB 481 CATGTGAAGGTTTAGAGACAGAAAGACAAAGATATCTACCTCAAGCTATATTTAAC 540  
QY 181 IleSerThrAspSerLeuGlnGlyLeuLeuTyrLeuValTrpValGlnAlaAlaAsn 200  
DB 541 ATCTCCACTGATTCATTAACAAGGTGCAAGAAAGATCTGTTGGGTCCCAAGACGCAAC 600  
QY 201 AlaLeuGlyMetGluSerLeuGlnLeuGlnIleHisIleLeuAspAspIleValIlePro 220  
DB 601 GCACTAGGCGATGAGAGATCAAAAACAATCACTGATGATATATAGTATCT 660  
QY 221 SerAlaAlaValIleSerArgAlaGluThrIleAsnAlaThrValProLeuThrIle 240  
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DB 781 ACAACCAAACTTGAATGTTTAAAGAAATTGACCAATTTTACATATGTGCAACACTCA 840  
QY 281 GluPheTyrLeuGluProAsnIleLeuTyrValPheGlnValArgCysGlnGluThrGly 300  
DB 841 GAATTTCACTTGAGCCAAACATTAACTAGCTATTTCAAGTGAATGTCAGAAACAGGC 900  
QY 301 LeuArgTyrTrpGlnProTyrPheSerSerProPhePheHisIleTyrProGluThrValPro 320  
DB 901 AAAAGATACAGGAGCCTTGAAGTCACTGTTTTCATATAAACACCTGAAACAGTTCCC 960  
QY 321 GlnValThrSerLeuAlaPheGlnHisAspThrTrpAsnSerGlyLeuThrValAlaSer 340  
DB 961 CAGGTCAATCAAAAGATTCACACATGACACACAGGAATTCCTGGGCTTAAACGTTGCTTC 1020  
QY 341 IleSerThrGlyHisLeuThrSerAspAsnArgIleAspIleGlyLeuLeuLeuGlyMet 360

DB 1021 ATCTTACAGGCGACCTTACTTCTGACAAACAGAGACACTTGGACTTTATTTGGGAATG 1080  
QY 361 IleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380  
DB 1081 ATCGCTTTGGCTGTATATGTTGCAATTCCTTCTTTATATGGGATATTTAAACAATCATTC 1140  
QY 381 ArgThrGlyIleLeuArgArgIleLeuLeuLeuIleProLeuSerTrpLeuTyrGluAspIle 400  
DB 1141 CGAATCGGATTTAAAGAAAGATCTTATTTGTTAATACAAAGTGGCTTTATGAAGATAT 1200  
QY 401 ProAsnMetLeuAsnSerAsnValIleLeuMetLeuGlnIleAsnSerGluLeuMetAsn 420  
DB 1201 CTTATATATGAAAACAGCAATGTTGTGAAAATCTCACGGAATAATGTGAATTAATGAAT 1260  
QY 421 AsnAsnSerSerGluGlnValLeuTyrValAspProMetIleThrGluIleLeuGluIle 440  
DB 1261 AATMAATTCAGTGAAGGCTCTATATGTTGATCCATGATTAACAGAGATMAAAGAAATC 1320  
QY 441 PheIleProGluHisIlePheProThrAspTyrTyrLeuGlyLeuAsnThrGlyProLeuGluThr 460  
DB 1321 TTCAATCCAGAACACAAAGCTTACAGACTACAAAGAGAAATACAGAACCCCTGGAGACA 1380  
QY 461 ArgAspTyrProGluAsnSerLeuPheAspAsnThrThrValValTyrIleProAspLeu 480  
DB 1381 AGAGACTACCCGCAAACTGCTATTGCACAATACTACAGTGTATATATCTCGATCTC 1440  
QY 481 AsnThrGlyTyrLeuProGlnIleSerAsnPheLeuProGluIleSerHisIleLeuSerAsn 500  
DB 1441 AATCACTGATATTAACCCCAATTTTCAAAATTTCTGCTGAGGAGAAAGCCATTCACGAAT 1500  
QY 501 AsnAsnGlnIleThrSerLeuThrLeuLeuProProValAspSerLeuAspSerGlyAsn 520  
DB 1501 AATMAATGAATTAATCTTCACTTAACCTTAACCAACAGTGAATCTTATAGCTCAGGAAT 1560  
QY 521 AsnProArgLeuGlnIleHisProAsnPheAlaPheSerValSerSerValAsnSerLeu 540  
DB 1561 AATCCAGGTTACAAAGACATCTAATTTTGTCTTTTCTGTTCAAGTGAATTCACATA 1620  
QY 541 SerAsnThrIlePheLeuGlyGluLeuSerLeuIleLeuAsnGlnGlyIleCysSerSer 560  
DB 1621 AGCAACACATATATTTCTTGAGAAATTAAGCTCATATTAATCAAGAGAAATCAGATCT 1680  
QY 561 ProAspIleGlnAsnSerValGluGluThrThrMetLeuLeuAsnAspSerPro 580  
DB 1681 CCGACATTAACAACTCAGAGAGAGAGAAACCAATGCTTTTGGAAAATGATTCACCC 1740  
QY 581 SerGluThrIleProGluGlnThrLeuLeuProAspGluPheValSerCysLeuGlyIle 600  
DB 1741 AGTGAATCATTTCCAAACAGACCTGCTTCCAGATGAATTTGCTCTTGGGGATC 1800  
QY 601 ValAsnGluGluLeuProSerIleAsnThrTyrPheProGlnAsnIleLeuGluSerHis 620  
DB 1801 GTGAATGAGAGATGCGCATCTATTAATTAATTTTCCAAATAATATTTGGAAAGCCAC 1860  
QY 621 PheAsnArgIleSerLeuLeuGlyLeu 629  
DB 1861 TTCATATGAGATTCACCTTGGAAAG 1887  
  
RESULT 8  
US-10-105-930-9  
; Sequence 9, Application US/10105930  
; Publication No. US20030009018A1  
; GENERAL INFORMATION:  
; APPLICANT: Maeda, Masateugu  
; APPLICANT: Yasuchi, No. US20030009018A1ko  
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12  
; FILE REFERENCE: 06501-105US1  
; CURRENT APPLICATION NUMBER: US/10/105, 930  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER: PCT/JP00/06654  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: JP 2000-240397



Db 1801 GTGATGAGAGAGTTCATCTATTATTTTCACAAAATATTTGGAAAGCCAC 1860  
Qy PheAsnArgIleSerLeuLeuGluLys 629  
Db 1861 TTCAATAGGATTTCACTCTTGGAAAG 1887

RESULT 9  
US-09-972-708-19  
; Sequence 19, Application US/09972708  
; Publication No. US2003005987A1  
; GENERAL INFORMATION:  
; APPLICANT: Immunex Corporation  
; APPLICANT: Cosman, David J.  
; APPLICANT: Mosley, Bruce A.  
; APPLICANT: Bird, Timothy A.  
; APPLICANT: Dubose, Robert F.  
; APPLICANT: Wiley, Steven R.  
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPR1 AND HPR2  
; FILE REFERENCE: 3160-B  
; CURRENT APPLICATION NUMBER: US/09/972,708  
; CURRENT FILING DATE: 2001-10-05  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 2830  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-972-708-19

Alignment Scores:  
Pred. No.: 0 Length: 2830  
Score: 3314.00 Matches: 626  
Percent Similarity: 99.5% Conservative: 0  
Best Local Similarity: 99.5% Mismatches: 3  
Query Match: 99.6% Indels: 0  
DB: 3 Gaps: 0

US-10-667-289-2 (1-629) x US-09-972-708-19 (1-2830)

Qy 1 MechAsn\*\*ValThrIleGlnThrPAspAlaValIleAlaLeuTyriIleLeuPheSerTrp 20  
Db 107 ATGATAGAGGTCACTATTTCATAGGATGACAGTAATACCCCTTTTCATATCTTCAGCTGG 166  
Qy 21 CysHieglYglYleThrAsnIleAsnCysSerGlyHisIleTrpValGluProAlaThr 40  
Db 167 TGCATAGAGGATTTACAAATATTAACCTGCTGGCCACATCGGAGAAACAGCCACA 226  
Qy 41 IlePheLysMetGlyMetAsnIleSerIleTyriCysGlnAlaAlaIleLysAsnCysGln 60  
Db 227 ATTTTAAAGATGGGTATGATATCTCTATATATGGCCAGAGCAATTAGAACTGCCAA 286  
Qy 61 ProArgLysLeuHisPheTyriLysAsnGlyIleLysGluArgPheGlnIleThrArgIle 80  
Db 287 CCAAGGAAACTCTATTTTATAAAATGGCATCAAAAGAAAGATTCAAAATCAACAGGATT 346  
Qy 81 AsnLysThrThrAlaArgLeuTrpTyriLysAsnPheLeuGluProHisAlaSerMetTyri 100  
Db 347 AATTAACCAACAAGCTGGCTTGGTATTAATAAATCTTCGGAACACATGCTTCATATAC 406  
Qy 101 CysThrAlaGluCysProLysHisPheGlnGluThrLeuIleCysGlyLysAspIleSer 120  
Db 407 TGCATGCTGATATGCCAAACATTTTCAGAGACACATGATATGGAAAAAGACATTTCT 466  
Qy 121 SerGlyTyriProProAspIleProAspGluValThrCysValIleTyriGluTyriSerGly 140  
Db 467 TCTGGATATCCGACAGATATCTCGATGAAGTAACCTGTGCATTTATGATATATTCGGC 526  
Qy 141 AsnMetThrCysThrTrpAsnAla\*\*LysLeuThrTyriIleAspThrLysTyriValIle 160  
Db 527 AACATGACTTGCACTGGAATGCTGGAGACTCACCTACATAGACAAATATAGCTGTA 586  
Qy 161 HisValLysSerLeuGluThrGluGluGlnGlnIleuThrSerSerTyriIleAsn 180

Db 587 CATGTGAAGATTAGAGACAGAAAGACCAACAGTATCTCACCTCAAGCTATATTAAAC 646  
Qy IleSerThrAspSerLeuGlnGlyLysTyriLeuValTrpValGlnAlaAlaAsn 200  
Db 647 ATCTCCACTGATTCATTAACAAGGTGGCAAGAAATCTTGGTTGGGTCCAAAGCGCAAC 706  
Qy 201 AlaLeuGlyMetGluGluSerLysGlnLeuGlnIleHisAlaLeuAspIleValIlePro 220  
Db 707 GCACTAGGACATGGAAGATCAAAAACAACCTCAAAATTCACCTGGATGATATAGTATACCT 766  
Qy 221 SerAlaAlaValIleSerArgAlaGluThrIleAsnAlaThrValProLysThrIleIle 240  
Db 767 TCTGCAGCCGCTATTTCCAGGCGCTGAGACATATAATCTCACAGGCCCAAGACCATATT 826  
Qy 241 TyrTrpAspSerGlnThrTrileGluLysValSerCysGluMetArgTyriLysAlaThr 260  
Db 827 TATTTGGATATGTCAAACAACTTGAAGAGTTTCTGTAAATGATATCAAGAGCTTACA 886  
Qy 261 ThrAsnGlnThrTrpAsnValLysGluPheAspThrAsnPheThrTyriValGlnGlnSer 280  
Db 887 ACAACCAAACTTGGAAATGTTAAAGATTTGACACCAATTTTCATATGTCACACATCA 946  
Qy 281 GluPheTyriLeuGluProAsnIleLysTyriValPheGlnValArgCysGlnGluThrGly 300  
Db 947 GAATTCTACTTGGAGCCAAACATTAAAGTACGTATTTCAAGTGAATGTCAAGAAACAGGC 1006  
Qy 301 LysArgTyriTrpGlnProTrpSerSerProPhePheHisIleTyriTrpGluThrValPro 320  
Db 1007 AAAAGTACTGGCAGCTTGAGTTCACGTCTTTTTCATTAACACCTGAAACGTTCC 1066  
Qy 321 GlnValThrSerLysAlaPheGlnHisAspThrTrpAsnSerGlyLeuThrValAlaSer 340  
Db 1067 CAGTGCATCATAAAGATTTCCAAACATGACATGAGATTCCTGGGTCAACAGTCTTCC 1126  
Qy 341 IleSerThrGlyHisLeuThrSerAspAsnArgGlyAspIleGlyLeuLeuLeuGlyMet 360  
Db 1127 ATCTCTACAGGACCTTACTTCTGACACAGAGAGACATTTGACATTTTATTTGGGATG 1186  
Qy 361 IleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380  
Db 1187 ATGCTCTTCTGTATGTTGTCATATCTTTCTTGTGATGGATATTTAACAGATCATTC 1246  
Qy 381 ArgThrGlyIleLysArgArgIleLeuLeuLeuIleProLysTrpLeuTyriGluAspIle 400  
Db 1247 CGAATCGGATTTAAAGAAAGATCTTATTTTAATCCAAAGTGGCTTTATGAAGATATT 1306  
Qy 401 ProAsnMetLysAsnSerAsnValValLysMetLeuGlnLysAsnSerGluLeuMetAsn 420  
Db 1307 CTTAATATGAATAAACAAGCAATGTTGTGAATAATGCTACAGAAATAAGTGAATGAAAT 1366  
Qy 421 AsnAsnSerSerGluGlnValIleuTyriValAspProMetIleThrGluIleLysGluIle 440  
Db 1367 AATTAATTCAGTAGCAGGCTCTATATGTTGATCCCATGATTCACAGAGTAAGAAATC 1426  
Qy 441 PheIleProGluHisLysProThrAspTyriLysLysGluAsnThrGlyProLeuGluThr 460  
Db 1427 TTCAATCCAGAAACACAGCTTACAGACTACAGAGAGAAATACAGAACCCCTGGAGACA 1486  
Qy 461 ArgAspTyriProGluAsnSerLeuPheAspAsnThrThrValValTyriIleProAspLeu 480  
Db 1487 AGAGACTACCCGCAAAATCGCTATTCGACAAATACTACAGTATATATCTCGATCTC 1546  
Qy 481 AsnThrGlyTyriLysProGlnIleSerAsnPheLeuProGluLysSerHisLeuSerAsn 500  
Db 1547 AACACTGGAATATAACCCCAAAATTTTCATAATTTCTCGTGAAGGAAGCCATCTCAGCAAT 1606  
Qy 501 AsnAsnGluIleThrSerLeuThrLeuLysProProValAspSerLeuAspSerGlyAsn 520  
Db 1607 AATATAGAAATATCTTCCCTTAACATTTAAACCAACGAGTTGATCTTGAAGCTCAGGAAT 1666  
Qy 521 AsnProArgLeuGlnLysHisProAsnPheAlaPheSerValSerSerValAsnSerLeu 540  
Db 1667 AATCCAGGTTACAAAGCATCTCAATTTTGTCTTTTCTGTTCAGATGGAATTCACATA 1726

QY 541 SerAsnThrIlePheLeuGlyGluLeuSerIleuIleuLeuGlnGlyGluCysSerSer 560  
Db 1727 AGCAACACAAATATTTCTTGAGAAATTAAGCCTCATATTAATCAAGAGATGAGTTCT 1786  
QY 561 ProAspIleGlnIleuSerValGluGlnGluThrThrMetLeuLeuGluIleuAsnAspSerPro 580  
Db 1787 CCGACACTTACAAAACCTAGTAGAGAGAGAAACCACTGCTTTGGAAAAATGATTCAACC 1846  
QY 581 SerGluThrIleProGluGlnThrLeuLeuProAspGluPheValSerCysLeuGlyIle 600  
Db 1847 AGTAAACATTCACAGAACAGACCCCTCTCTGATGATGATTTGCTCTCTGTTGGGATC 1906  
QY 601 ValAsnGluGluLeuProSerIleAsnThrThrPheProGlnAsnIleLeuGluSerHis 620  
Db 1907 GTGAATGAGAGGTGCATCATTAATATTAATTTTCCAAAATATTTGGAAAGCCAC 1966  
QY 621 PheAsnArgIleSerLeuLeuGluLys 629  
Db 1967 TTCAAATAGATTTCATCTTGAAAAAG 1993

## RESULT 10

US-10-715-667-19  
/ Sequence 19, Application US/10715667  
/ Publication No. US20040152161A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Immunex Corporation  
/ APPLICANT: Cosman, David J.  
/ APPLICANT: Mosley, Bruce A.  
/ APPLICANT: Bird, Timothy A.  
/ APPLICANT: Dubose, Robert F.  
/ APPLICANT: Wiley, Steven R.  
/ TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2  
/ FILE REFERENCE: 3160-B  
/ CURRENT APPLICATION NUMBER: US/10/715, 667  
/ PRIOR FILING DATE: 2003-11-14  
/ PRIOR APPLICATION NUMBER: US/09/972, 708  
/ NUMBER OF SEQ ID NOS: 29  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 19  
/ LENGTH: 2830  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
US-10-715-667-19

## Alignment Scores:

Pred. No.: 0 Length: 2830  
Score: 3314.00 Matches: 626  
Percent Similarity: 99.5% Conservative: 0  
Best Local Similarity: 99.5% Mismatches: 3  
Query Match: 99.6% Indels: 0  
DB: 8 Gaps: 0

US-10-667-289-2 (1-629) x US-10-715-667-19 (1-2830)

QY 1 MetAsn\*\*ValThrIleGlnTrpAspAlaValIleAlaLeuTyrlleLeuPheSerTrp 20  
Db 107 ATGAATCAGGTCACTATTCATAGGATGCGAGTAATACCCCTTTCATACATCTTCAGCTGG 166  
QY 21 CysHleGlyGlyIleThrAsnIleAsnCysSerGlyHisIleTrpValGluProAlaThr 40  
Db 167 TGTCAATGAGAAATTACAAATATATTAACGTCTGCGCAATCTGGTAGAACCGACCA 226  
QY 41 IlePheIleMetGlyMetAsnIleSerIleTyrcyGlnIleAlaIleIleValAsnCysGln 60  
Db 227 ATTTTAAAGAGGATGAATATCTCTATATATGCGAAGAGCAATTAAGAACTGCGCAA 286  
QY 61 ProArgIleLeuHisPheTyrlleAsnGlyIleIleGluArgPheGlnIleThrArgIle 80  
Db 287 CCAAGGAAATCTCTTTTATTAATAAATGCGATCAAAAGAAATTTCAATCAACAAGATT 346  
QY 81 AsnIleThrThrAlaArgLeuTrpTyrlleAsnIleLeuGluProHisAlaSerMetTyrlle 100

Db 347 AATTAACCAACACCTGGCTTTGTATTAATAAATCTTCTGGAACACATGCTTCTATGTAC 406  
QY 101 CysThrAlaGluCysProLysHisPheGlnGluThrLeuIleCysGlyLysAspIleSer 120  
Db 407 TGCATCTCTGAATATCTCCAAACATTTTCAAGAGACATGATATGTGAAAAAGCATTTCT 466  
QY 121 SerGlyTyrlleProAspIleProAspGluValIleCysValIleTyrlleGlyTyrlle 140  
Db 467 TCTGGATATCTCGCAATATTTCTGATGAAGTAACCTGTGTCTATTAATATTCAGGC 526  
QY 141 AsnMetThrCysThrThrPheAla\*\*\*LysLeuThrTyrlleAspHisTyrlleValIle 160  
Db 527 AACATGACTTGACCTGGAAATGCTGGAACTCACTACATTAACCAAAATATGAGTA 586  
QY 161 HisValIleSerLeuGluThrArgIleGluGlnGlnIleTyrlleThrSerSerTyrlleAsn 180  
Db 587 CATGTGAAGAGTTTAGAGACAGAAAGAACCAAGATATTCACCTCAACTATATTAAC 646  
QY 181 IleSerThrAspSerLeuGlnGlyLysLysTyrlleValIleTrpValGlnAlaIleAsn 200  
Db 647 ATCTCCACTGATTCATTAACAAGGTGGCAAGATGACTGTGGTTGGGTCCAAAGCAAC 706  
QY 201 AlaLeuGlyMetGluGluSerLysGlnLeuGlnIleHisIleuAsnAspIleValIlePro 220  
Db 707 GCACTAGGACATGGAAGATCAAAACACCTGCAAAATTCACCTGATGATATAGATACCT 766  
QY 221 SerAlaAlaValIleSerArgAlaGluThrIleAsnAlaThrValProLysThrIleIle 240  
Db 767 TCTGCAAGCCCTCATTTTCCAGGCTGAGACATATAATCTCACTGCGCAAGACATATT 826  
QY 241 TyrlleAspSerGlnThrThrIleGlyLysValSerCysGluMetArgTyrlleAsnThr 260  
Db 827 TATTTGGATGTGCAACAATGAAAGTTGAAAGTTTCCGTGTAATGAGATCAAGGCTACA 886  
QY 261 ThrAsnGlnThrThrPheValIleGluPheAspThrAsnPheThrTyrlleGlnIleSer 280  
Db 887 ACAACCAAACTTGAATGTAAAGAAATTTGAACCAATTTTCAATATGTGCAACAGTCA 946  
QY 281 GluPheTyrlleGluProAsnIleLysTyrlleValPheGlnValArgCysGlnGluThrGly 300  
Db 947 GAATTCCTACTGAGGCCAAACATTAAGTACGTATTTCACTGATGATGATCAAGAAACAGC 1006  
QY 301 LysArgTyrlleTrpGlnProTrpSerSerProPheHisLysThrProGluThrValPro 320  
Db 1007 AAAAGTACTGGACCTTGAGTTCACTGTTTTCATTAACACCTGAAACAGTTCCC 1066  
QY 321 GlnValThrSerLysAlaPheGlnHisAspThrTrpAsnSerGlyLeuThrValAlaSer 340  
Db 1067 CAGGTCAATCAAAAGCAATTCACAATGACATGGAATTTCTGGCTTAACAGTTGCTTC 1126  
QY 341 IleSerThrGlyHisLeuThrSerAspAsnArgIleAspIleGlyLeuLeuGlyMet 360  
Db 1127 ATCTTCAAGGACCTTACTTCTTGACACAGAGAGACATTTGACTTTTATTTGGAAATG 1186  
QY 361 IleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380  
Db 1187 ATCGTCTTCTGTATGTTGCAATTTCTTTGATGGATATTAACATCATTC 1246  
QY 381 ArgThrGlyIleLysArgAlaGlyIleLeuLeuIleProLysTrpLeuTyrlleGluAspIle 400  
Db 1247 CGAACTGGAGTTAAAGAAAGATCTTAATGTAAATACCAAAAGTGGCTTAATGAAGAAATT 1306  
QY 401 ProAsnMetLysAsnSerAsnValAlaLysMetLeuGlnIleuAsnSerGluLeuMetAsn 420  
Db 1307 CTTAATATGAAGAAACAGCAATTTGTGAAATGCTACAGAAATATGTAATCATTAAT 1366  
QY 421 AsnAsnSerSerGluGlnValLeuTyrlleAspProMetIleThrGluIleLysGluIle 440  
Db 1367 AATTAATTCAGTGAAGGTCTATATATGTTGATCCCATGATTAACAGAGATAAAGAAATC 1426  
QY 441 PheIleProGluHisLysProThrAspTyrlleLysGluAsnThrGlyProLeuGluThr 460

Db 1427 TTCATCCAGAACAAAGCCTTACAGACTACAAAGAGGATACAGAGCCCTTGAGACA 1486  
Qy 461 ArgAspTyrProGlnIaenSerLeuPheAspAsnThrValIleTyrIleProAspLeu 480  
Db 1487 AGAAGTACCCGCAAACTCGCTATTCAGCAATACACAGTGTATATATTCCTGATCTC 1546  
Qy 481 AsnThrGlyTyrIleProGlnIleSerAsnPheLeuProGluGlySerHisIleLeuSerAsn 500  
Db 1547 AACCTGATATTAACCCCAATTTCAATTTTCTGCTGAGGAGACGACATCAGCAAT 1606  
Qy 501 AsnAsnGluIleThrSerLeuThrLeuIleProProValAspSerLeuAspSerGlyAsn 520  
Db 1607 AATATGAAATTAATCTTCACTTAACCTTAACCAACAGATGATCTTGAAGTCAAGAAAT 1666  
Qy 521 AspProGluLeuGlnIlePheProAsnPheIlePheSerValSerSerValAsnSerLeu 540  
Db 1667 AATCCAGGTATCAAAAGCATCTTAATTTGCTTTTCTGTTCAAGTGAATTCACATA 1726  
Qy 541 SerAsnThrIlePheLeuGlyGluLeuSerLeuIleLeuAsnGlnIleGluGlySerSer 560  
Db 1727 AGCAACACANATTTCTTGAGATTAAGCCTCATATTAATCAAGAGATGACATTCCT 1786  
Qy 561 ProAspIleGlnAsnSerValGluGluGluThrThrMetLeuLeuGluAsnAspSerPro 580  
Db 1787 CCTGACATACAAACTCAGTATGAGAGAGAAACCAACATGCTTTTGAAATGATTCACCC 1846  
Qy 581 SerGluThrIleProGluGlnIleLeuLeuProAspGluPheValSerCysLeuGlyIle 600  
Db 1847 AGTAAACTATTCAGAAACAGACCCCTGCTGTATGATAATTTGCTCTGTTGGAGATC 1906  
Qy 601 ValAsnGluGluLeuProSerIleAsnThrTyrPheProGlnIleLeuGlySerHis 620  
Db 1907 GTGATATGAGAGTGGCCATCATTAATTAATTTTCCACAAATATTTTGGAAAGCCAC 1966  
Qy 621 PheAsnArgIleSerLeuLeuGlyLeu 629  
Db 1967 TTCATATGATTTCACTCTTGAAAG 1993

RESULT 11  
US-10-105-930-5  
; Sequence 5, Application US/10105930  
; Publication No. US20030009018A1  
; GENERAL INFORMATION:  
; APPLICANT: Maeda, Masatsugu  
; TITLE OR INVENTION: NOVEL HEMOPOLYMERIN RECEPTOR PROTEIN, NR12  
; FILE REFERENCE: 06501-105US1  
; CURRENT APPLICATION NUMBER: US/10/105, 930  
; PRIOR FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER: PCT/JP00/06654  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: JP 2000-240397  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: JP 11-273358  
; PRIOR FILING DATE: 1999-09-27  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PASTESEQ for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 2123  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (98) ... (1984)  
US-10-105-930-5

Alignment Scores:  
Pred. No.: 0 Length: 2123  
Score: 3292.00 Matches: 622  
Percent Similarity: 99.2% Conservative: 2  
Best Local Similarity: 98.9% Mismatches: 5  
Query Match: 99.0% Indels: 0  
DB: 6 Gaps: 0

US-10-667-289-2 (1-629) x US-10-105-930-5 (1-2123)  
Qy 1 MetAsn\*\*\*ValThrIleGlnIleProAspAlaValIleIleLeuTyrIleLeuPheSerTyr 20  
Db 98 ATGATTAAGGTCTATTCATTAAGGATGAGATTAATACCCCTTATCATATCTTCAAGCTGG 157  
Qy 21 CysHisGlyIleIleThrAsnIleAsnCysSerGlyHisIleTyrPheValGluProAlaThr 40  
Db 158 TGTCTATGAGAGATTAACAAATTAATTAATCTGCTGCGCAACATCTGGATGAGAACCGACA 217  
Qy 41 IlePheIleSerGlyMetAsnIleSerIleTyrCysGlnAlaAlaIleIleAsnCysGln 60  
Db 218 ATTTTAAATGAGGTGTGAATATCTCATATTAATGCGAACAGCAATTAAGAACTGCCAA 277  
Qy 61 ProArgIleLeuHisPheTyrIleAsnGlyIleIleGluIleThrPheGlnIleThrArgIle 80  
Db 278 CCAAGGAACCTTCAATTTTAATAAATGGATCAAAAGAAATTTCAAAATCAAGAGATT 337  
Qy 81 AsnIleThrThrAlaArgLeuTyrTyrIleAsnPheLeuGluProHisAlaSerMetTyr 100  
Db 338 AATTAACAAACACTCGGCTTTGGTATTAATACTTTCTGGAACCAACATGCTTCTATGTAC 397  
Qy 101 CysThrAlaGluCysProIleHisPheGlnIleThrIleIleCysGlyIleAspIleSer 120  
Db 398 TGCACCTGTAATGTCCCAAAACATTTTCAAGAGACACTGATATGTGAAAAAGACATTTCT 457  
Qy 121 SerGlyTyrProProAspIleProAspGluValThrCysValIleTyrGlyTyrSerGly 140  
Db 458 TCTGATATCCGCAAGTATTCCTGATGAGATTAACCTGTCTCATTTATGAAATATTCAGGC 517  
Qy 141 AsnMetThrCysThrTyrPheAlaIle\*\*\*IleLeuThrTyrIleAspThrIleValIle 160  
Db 518 AACATGACTTGCACTGGAATGCTGGAGGCTCACTCAATAGACAAATACGTGTGTA 577  
Qy 161 HisValIleSerLeuGlnIleThrGluGlnIleGlnIleThrLeuThrSerSerTyrIleAsn 180  
Db 578 CATGTGAAGATTTAAGACAGAAAGAGCAACAGATCATCTCACTCAAGCTATATTAAC 637  
Qy 181 IleSerThrAspSerLeuGlnIleGlyIleIleValTyrIleValIleGlnAlaIleAsn 200  
Db 638 ATCTCCACTGATTCATTAACAGGTGGCAGAAAGTATGTTGGTGGCCAGACGCAAC 697  
Qy 201 AlaLeuGlyMetGluSerIleGlnIleGlnIleIleHisIleAsnAspAlaIleValIlePro 220  
Db 698 GCATAGGACGTGAAGAGTCAAAACATCTCAAAATTCACCTGATGATATATGATATCTT 757  
Qy 221 SerAlaIleValIleSerArgAlaGluThrIleAsnAlaThrValProIleThrIleIle 240  
Db 758 TCTGCAAGCGCTATTTCCAGGGCTGAGACTATTAATGCTACAGTGGCCAAAGACATATTT 817  
Qy 241 TyrTyrAspSerGlnThrIleGluIleValIleSerCysGluMetCysGlyIleValIleThr 260  
Db 818 TATTTGGATATGTCAAACAAATTTGAAGATTTCCGTGTAATATGATATCAAGGTACA 877  
Qy 261 ThrAsnGlnThrTyrAsnValIleGluPheAspThrAsnPheThrTyrValIleGlnIleSer 280  
Db 878 ACAAAACCAACTTGAATGTATTAAGATTTGACACCAATTTTACATATATGTCACATCA 937  
Qy 281 GluPheTyrLeuGluProAsnIleIleTyrValIlePheGlnValIleArgCysGlnIleThrGly 300  
Db 938 GAATTCATCTTGAGCCCAACATTAAGTACGTATTTCAAGTGAATGTCAAGAAACAGGC 997  
Qy 301 LysArgTyrTyrGlnProTyrPheSerSerProPhePheHisIleThrProGluThrValPro 320  
Db 998 AAAAGTACTGCGAGCTTGAAGTTCACGTGTTTTTTCATTAACACCTGAAGACGTTCCC 1057  
Qy 321 GluValThrSerIleValIlePheGlnHisAspThrTyrAsnSerGlyLeuThrValAlaSer 340  
Db 1058 CAGGTCAATCAAAAGATTCACATGACATGACATGAAATTTCTGGGCTTAACAGTTGCTTCC 1117  
Qy 341 IleSerThrGlyHisLeuThrSerAspAsnArgIleAspIleGlyLeuLeuGlyMet 360



Db 1118 ATCTTACAGGGACCTTACTTGTGACACAGAGACATTGGACTTTTATTTGGGAATG 1177  
 Qy 361 ILeValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380  
 Db 1178 ATGCTCTTGTCTGTATGTTGTCAATCTTTCTTTGATTTGGACATTTTACAGATCTTC 1237  
 Qy 381 ArgThrGlyIleValArgArgIleLeuLeuLeuIleProlySerPleuYrGluAspIle 400  
 Db 1238 CGAACTGGAGTTAAAGAGATCTTATTTGTAATACCAAGTGGCTTTATGAAATATT 1297  
 Qy 401 ProAsnMetLysAsnSerAsnValValLysMetLeuIleGluAsnSerGluLeuMetAsn 420  
 Db 1298 CCTATATGAAAAACACAAATGTTGTAAATGTCTACAGAAATAGTGAATCTTATTAAT 1357  
 Qy 421 AsnAsnSerSerGluGluValLeuYrValAspProMetIleThrGluIleGluIle 440  
 Db 1358 AATTAATTCAGTGGAGAGCTCTTATGTTGATTCCTGATTCAGAGATTAAGAAATC 1417  
 Qy 441 PheIleProGluIleValSerProThrAspYrIleValSerGluAsnThrGlyProLeuGluThr 460  
 Db 1418 TTCTATCCCAAGACCAAGCCTACAGACTACAGAGAGAAATACAGAGACCCCTGGAGACA 1477  
 Qy 461 ArgAspYrProGluAsnSerLeuPheAspAsnThrValValYrIleProAspLeu 480  
 Db 1478 AGAGACTACCCGCAAACTGCTATTCAGCAATACACAGTTGATATATTCCTGATCTC 1537  
 Qy 481 AsnThrGlyYrIleYrProGluIleSerAsnPheLeuProGluGluSerIleLeuSerAsn 500  
 Db 1538 AACCTGATATTAACCCCAATTTTCAATTTTCTGCTGAGGAGAACCTTCAGTAT 1597  
 Qy 501 AsnAsnGluIleThrSerLeuThrLeuLysProProValAspSerLeuAspSerGlyAsn 520  
 Db 1598 AATATGAAATTAATCTTCTTAACACTTAACCAACAGATGATCTTACAGACTCAGAAAT 1657  
 Qy 521 AspProGluGluGluValSerProAsnPheAlaPheSerValSerSerValAsnSerLeu 540  
 Db 1658 AATCCAGGTTCACAAAGCATCTTAATTTTGTCTTTCTGTTCAAGTGAATTCCTA 1717  
 Qy 541 SerAsnThrIlePheLeuGlyGluLeuSerLeuIleLeuAsnGluGlyGluYrSerSer 560  
 Db 1718 AGCAACACATATTTCTTGAAGATTAAGCTCTCATATTAATCAAGAGAAATGCAATCT 1777  
 Qy 561 ProAspIleGluAsnSerValGluGluGluThrThrMetLeuLeuGluAsnAspSerPro 580  
 Db 1778 CCTGACATACAAACTCAGTACAGAGAGAAACCACTGCTTTGAAAAATGATTCACCC 1837  
 Qy 581 SerGluThrIleProGluGluThrLeuLeuProAspGluPheValSerGlyLeuGlyIle 600  
 Db 1838 AGTAAACTATTTCCAGAACAGACCTGCTCTGATGATAATTTGCTCTGTTGGGATC 1897  
 Qy 601 ValAsnGluGluLeuProSerIleAsnThrYrPheProGluAsnIleLeuGluSerHis 620  
 Db 1898 GTGAATAGAGAGTTGCCATCTATTAATCTTATTTCCACAAATATTTTGGAAAGCCAC 1957  
 Qy 621 PheAsnArgIleSerLeuLeuGluLys 629  
 Db 1958 TTCAATAGGATTTCACTTGGAAAAAG 1984

RESULT 12  
 US-09-972-708-22  
 ; Sequence 22, Application US/09972708  
 ; Publication No. US20030059871A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Immune Corporation  
 ; APPLICANT: Cosman, David J.  
 ; APPLICANT: Mosley, Bruce A.  
 ; APPLICANT: Bird, Timothy A.  
 ; APPLICANT: Dubose, Robert F.  
 ; APPLICANT: Wiley, Steven R.  
 ; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2  
 ; FILE REFERENCE: 3160-B  
 ; CURRENT APPLICATION NUMBER: US/09/972, 708  
 ; CURRENT FILING DATE: 2001-10-05

; NUMBER OF SEQ ID NOS: 29  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 22  
 ; LENGTH: 1698  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-972-708-22  
 Alignment Scores:  
 Pred. No.: 0 Length: 1698  
 Score: 2952.00 Matches: 562  
 Percent Similarity: 89.3% Conservative: 3  
 Best Local Similarity: 89.3% Mismatches: 64  
 Query Match: 88.8% Indels: 64  
 DB: 3 Gaps: 1  
 US-10-667-289-2 (1-629) x US-09-972-708-22 (1-1698)  
 Qy 1 MetAsn\*\*\*ValThrIleGlnTrpAspAlaValIleAlaLeuYrIleLeuPheSerTrp 20  
 Db 1 ATGAATCAGGTGACTATTCATATGGAGATGCAAGTATAGCCCTTTACATACATCTGAG 60  
 Qy 21 CysHisGlyGlyIleThrAsnIleAsnCysSerGlyHisIleTrpValGluProAlaThr 40  
 Db 61 TGTCAAGAGAGAAATACAAATATTAACCTGCTGGCCACATCTGGGTAGAACAGCCACA 120  
 Qy 41 ILePheLysMetGlyMetAsnIleSerIleYrCysGluAlaAlaIleLysAsnCysGln 60  
 Db 121 ATTTTAAAGTGGATTAATATCTCATATATTTGGCAACACACAAATTAAGACTGGCAA 180  
 Qy 61 ProArgLysLeuHisPheYrLysAsnGlyIleLysGluArgPheGluIleThrArgIle 80  
 Db 181 CCAAGGAACTTCAATTTTATTAATAAATGGCATCAAGAAAGATTTCAATCACAAGATT 240  
 Qy 81 AsnLysThrThrAlaArgLeuTrpYrLysAsnPheLeuGluProHisAlaSerMetYr 100  
 Db 241 AATTAACCAACACACTGCTTGTGATTAATAAATCTTGTGAACACATGCTTCTATGTAC 300  
 Qy 101 CysThrAlaGluCysProLysHisPheGluGluThrLeuIleCysGlyLysAspIleSer 120  
 Db 301 TGCATGCTGAAATGTCCTCAAACTTTTCAAGACACCTGATATGTGAAAAAGCATTTCT 360  
 Qy 121 SerGlyYrProProAspIleProAspGluValThrCysValIleYrGluYrSerGly 140  
 Db 361 TCTGATATCTGGCAGATATCTCTGATGAAAGTACCTGTCTATTAATATTTACAGGC 420  
 Qy 141 AsnMetThrCysThrTrpAsnAla\*\*\*LysLeuThrYrIleAspThrLysYrValVal 160  
 Db 421 AACATGCTTGACCTGGAAATGCTGGAACTCACTACATAGACACAAATACGTGTGTA 480  
 Qy 161 HisValLysSerLeuGluThrGluGluGluGluGluGluGluGluGluGluGluGluGlu 180  
 Db 481 CATGTGAAGAGTTTAAAGACAGAAAGAGCAACAGTATCTCACTCAACATATTAATAC 540  
 Qy 181 ILeSerThrAspSerLeuGluGlyLysLysYrLeuValTrpValGluAlaAlaAsn 200  
 Db 541 ATCTCCACTGATTCATTAACAAGGTGGCAAGAAATGTAATGTTGGGTCCAGACGAAAC 600  
 Qy 201 AlaLeuGlyMetGluGluSerLysGluGluGluGluGluGluGluGluGluGluGluGlu 220  
 Db 601 GCACTAGGACATGAGAGAGTCAAAACACATGCAAAATTCACCTGATATATATAGATACCT 660  
 Qy 221 SerAlaAlaValIleSerArgAlaGluThrIleAsnAlaThrValProLysThrIleIle 240  
 Db 661 TCTGACGCTGATTTCCAGAGGCTGAGACATTAATCTCACTGACCCCAAGACATTAAT 720  
 Qy 241 TyrTrpAspSerGluThrIleGluLysValSerCysGluMetArgYrLysAlaThr 260  
 Db 721 TATTGGATAGTCAACCAATTTGAAAGTTTCCGTGTAATATGAGATCAAGGCTACCA 780  
 Qy 261 ThrAsnGluThrTrpAsnValLysGluPheAspThrAsnThrYrValGluGlnSer 280  
 Db 781 ACAACCAACCTGGAAATGTTAAAGAAATTTGACCAATTTTACATATGTGCAACAGTCA 840



QY 281 GluPheTyrLeuGluProAsnIleValPheGlnValArgCysGlnGluThrGly 300  
DB 841 GAATTCACCTGGAGCCAACTTAAGTACCTATTCAAGAGCATGTCAAGAAACAGGC 900  
QY 301 LysArgTyrTrpGlnProTyrSerSerProPhePheHisValThrProGluThrValPro 320  
DB 901 AAAAGGACTGGAGCCCTGGAGTTCACTGTTTTCATATAAACAACCTGAA----- 951  
QY 321 GlnValThrSerValPheGlnHisAspThrTrpAsnSerGlyLeuThrValAlaSer 340  
DB 951 ----- 951  
QY 341 IleSerThrGlyHisLeuThrSerAspAsnArgGlyAspIleGlyLeuLeuGlyMet 360  
DB 951 ----- 951  
QY 361 IleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380  
DB 951 ----- 951  
QY 381 ArgThrGlyIleLysValGArgGlyLeuLeuLeuIleProLysTrpLeuTyrGlyAspIle 400  
DB 952 ---ACAGGATTAAGAAAGAGATCTTATGTTAATACCAAGTGGCTTTATGAAAGATATT 1008  
QY 401 ProAsnMetLysAsnSerAsnValValLysMetLeuGlnGlnAsnSerGlyLeuMetAsn 420  
DB 1009 CCTAATATGAAAAACACCAATGTTGTAAAAATGTACAGAAATAGTAACTTATGAAAT 1068  
QY 421 AsnAsnSerSerGlnGlnValLeuTyrValAspProMetIleThrGlnIleLysGlnIle 440  
DB 1069 AATTAATTCAGTGGAGCGCTCTATGTTGATGCTCATGATTCAGAGATTAAGAAATC 1128  
QY 441 PheIleProGluHisLysProThrAspTyrLysLysGlnAsnThrGlyProLeuGluThr 460  
DB 1129 TTCAATCCCAAGAACCAAGCCTACAGCTACAGAAAGAGAAATACAGACCCCTGGAGACA 1188  
QY 461 ArgAspTyrProGlnAsnSerLeuPheAspAsnThrValValTyrIleProAspLeu 480  
DB 1189 AGAGACTACCGCAAACTGCTATGACAAATACAAAGTGTATATATTCCTGATCTC 1248  
QY 481 AsnThrGlyTyrLysProGlnIleSerAsnPheLeuProGluGlySerHisLeuSerAsn 500  
DB 1249 AACCACTGATATTAACCCCAATTTTCAATTTTCTGCTGAGGAGAACCATCTAGCAAT 1308  
QY 501 AsnAsnGluIleThrSerLeuThrLeuLysProProValAspSerLeuAspSerGlyAsn 520  
DB 1309 AATTAATGAAATTACTTCTTAACACTTAACACACAGTGTCTTACAGCTCAGAAAT 1368  
QY 521 AsnProArgLeuGlnLysHisProAsnPheAlaPheSerValSerSerValAsnSerLeu 540  
DB 1369 AATCCCAAGTTTACAAAGCAATCTTAATTTGCTTTTCTGTTCAAGTGTGAATTCATA 1428  
QY 541 SerAsnThrIlePheLeuGlyGluLeuSerLeuIleLeuAsnGlnGlyGluCysSerSer 560  
DB 1429 AGCAACACATATTTCTTGGAGAAATTAAAGCTCATATTAATCAAGAGATGCAATCTT 1488  
QY 561 ProAspIleGlnAsnSerValGluGluGluThrThrMetLeuLeuGluAsnAspSerPro 580  
DB 1489 CCGTACATACAAACCTAGTAGAGAGAGAAACCACTGCTTTGGAAAAATGATTCACCC 1548  
QY 581 SerGluThrIleProGluGlnThrLeuLeuProAspGluPheValSerGlyLeuGlyIle 600  
DB 1549 AGTGAACCTATTCAGAACAGACCCCTGCTTCGATGAATTTGCTCTGTTGGGGATC 1608  
QY 601 ValAsnGluGluLeuProSerIleAsnThrTyrPheProGlnAsnIleLeuGluSerHis 620  
DB 1609 GTGAGTAGAGAGTTGCCATCTATTAATCTTATTTCCACAAATATTTTGGAAAGCAC 1668  
QY 621 PheAsnArgIleSerLeuLeuGluLys 629  
DB 1669 TTCATATGAGATTCACCTTGGAAAG 1695

RESULT 13  
US-10-715-667-22  
; Sequence 22. Application US/10715667  
; Publication No. US20040152161A1  
; GENERAL INFORMATION:  
; APPLICANT: Immunex Corporation  
; APPLICANT: Cosman, David J.  
; APPLICANT: Mosley, Bruce A.  
; APPLICANT: Bird, Timothy A.  
; APPLICANT: Dubose, Robert F.  
; APPLICANT: Wiley, Steven R.  
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPR1 AND HPR2  
; FILE REFERENCE: 3160-B  
; CURRENT APPLICATION NUMBER: US/10/715,667  
; CURRENT FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: US/09/972,708  
; PRIOR FILING DATE: 2001-10-05  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 22  
; LENGTH: 1698  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-715-667-22  
  
Alignment Scores:  
Pred. No.: 0 Length: 1698  
Score: 2952.00 Matches: 562  
Percent Similarity: 89.3% Conservative: 0  
Best Local Similarity: 89.3% Mismatches: 3  
Query Match: 88.8% Indels: 64  
DB: Gaps: 1  
  
US-10-667-289-2 (1-629) x US-10-715-667-22 (1-1698)  
QY 1 MetAsn\*\*ValThrIleGlnTrpAspAlaValIleAlaLeuTyrIleLeuPheSerTrp 20  
DB 1 ATGAATCAGGTCACTATTCATGAGATGAGATAGCCCTTACATACACTTCAGCTGG 60  
QY 21 CysHisGlyGlyIleThrAsnIleAsnCysSerGlyHisIleTrpValGluProAlaThr 40  
DB 61 TGTCAAGAGAAATTCAAATATTAATCTGCTGGCCACATCTGGGTAGAACCAAGCCACA 120  
QY 41 IlePheLysMetGlyMetAsnIleSerIleTyrCysGlnAlaAlaIleLysAsnCysGln 60  
DB 121 ATTTTAAAGTGGGTATGATATCTCTATATATTCACACCAATTAAGAACTGCCAA 180  
QY 61 ProArgLysLeuHisPheTyrLysAsnGlyIleLysGluArgPheGlnIleThrArgIle 80  
DB 181 CCAAGGAATCTCATTTTATTAATAAATGGCATCAAGAAAGAAATTCAAATCACAAGATT 240  
QY 81 AsnLysThrThrAlaArgLeuTyrTyrLysAsnPheLeuGluProHisAlaSerMetTyr 100  
DB 241 AATTAACCAACACACTCGCTTGTGTATTAATAAATCTTCTGGAACACATGCTTATGTAC 300  
QY 101 CysThrAlaGluCysProLysHisPheGlnGluThrLeuIleCysGlyLysAspIleSer 120  
DB 301 TGCATCTGCAATGCTCCAAACATTTTCAAGAACACTGATATGAGAAAGACATTTCT 360  
QY 121 SerGlyTyrProProAspIleProAspGluValThrCysValIleTyrGlyTyrSerGly 140  
DB 361 TCTGATATCCGCAATATCTCTGATGAAGTAACTGTCATTTATGAATATTCAGGC 420  
QY 141 AsnMetThrCysThrTrpAsnAla\*\*LysLeuThrTyrIleAspThrLysValVal 160  
DB 421 AACATGACTTGCACTCGGAATGCTGGAGCTCACCATTACCTAACCAAAATACGTGTA 480  
QY 161 HisValLysSerLeuGlnTrpGluGluGluGlnGlnGlyThrLeuThrSerSerTyrIleAsn 180  
DB 481 CATGTGAAGGTTTAGAGACAGAAAGAACCAAGTATTCACCTCAGCTATATTAC 540  
QY 181 IleSerThrAspSerLeuGlnGlyLysLysTyrLeuValTrpValGlnAlaAlaAsn 200

Db 541 ATCTCAGTATTCATTACAAAGTGGCAAGAGTACTGGTTGGTCCAGCAAGCAAC 600  
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 Db 601 GCATCAGGATGGAAGAGTCAAAACCTGCAATTCACCTGAGATGATATAGTATCCT 660  
 Qy 221 SerAlaValileSerArgAlaGluThrileAsnAlaThrValProLySerThrile 240  
 Db 661 TCTGCAACCCGTCATTTCCAGGGCTGAGACTATAATCTACAGGCCCAAGACCATAT 720  
 Qy 241 TTTTThpAspSerGlnThrThrileGluValSerCyseGluMetArgTyrValileThr 260  
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 Db 781 ACAACCAAACTGGAAATGTTAAAGATTTGACCCAAATTTTACATATGTCACACATCA 840  
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 Qy 301 LyserArgTyrTrpGlnProTyrPserSerProPhePheHislyserThrProGluThrValPro 320  
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 Qy 321 GlnValThrSerLySalPheGlnHisAspThrTrpAsnSerGlyLeuThrValAlaSer 340  
 Db 951 ----- 951  
 Qy 341 IleSerThrGlyHisleuThrSerAspAsnArgGlyAspIleGlyLeuLeuGlyMet 360  
 Db 951 ----- 951  
 Qy 361 IleValPheAlaValMetLeuSerIleLeuSerIleGlyIlePheAsnArgSerPhe 380  
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 Db 952 -----ACAGGATTAAGAAAGATCTTATTTGTTATACCAAGTGGCTTTATGAAGATATT 1008  
 Qy 401 ProAsnMetLyserAsnSerAsnValileLyseMetLeuGlnLeuAsnSerGluLeuMetAsn 420  
 Db 1009 CCTATATGAAACCAAGCAATGTTGTGAAATGCTACAGAAATAGTGAACCTTATGAAAT 1068  
 Qy 421 AsnAsnSerSerGluGlnValileuTyrValAspProMetIleThrGluIleGluIle 440  
 Db 1069 AATATATTCAGTGAAGAGTCTATATGTTGATCCCATGATTTACAGAGATTAAGAAATC 1128  
 Qy 441 PheIleProGluHislyserProThrAspTyrLyserLyseGluAsnThrGlyProLeuGluThr 460  
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 Qy 501 AsnAsnGluIleThrSerLeuThrLeuLyserProValAspSerLeuAspSerGlyAsn 520  
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 Qy 541 SerAsnThrIlePheLeuGlyGluLeuSerIleuLeuAsnGlnGlyGlyCyseSerSer 560  
 Db 1429 AGCAACACAAATATTTCTTGAGAAATTAAAGCTCATATTAATCAAGAGAAATGCAATTC 1488

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 Db 1489 CCGACATCAAAACCTCAGTGAAGAGAGAAACCAACCATGCTTTTGGAAAAATGATTCACCC 1548  
 Qy 581 SerGluThrIleProGluGlnThrLeuLeuProAspGluPheValileSerCyseLeuGlyIle 600  
 Db 1549 AGTGAACATATTCACAAACAGACCCCTGCTTCGATGAATTTGTCTCTGTTTGGGGATC 1608  
 Qy 601 ValAsnGluGluLeuProSerIleAsnThrTyrPheProGlnAsnIleLeuGluSerHis 620  
 Db 1609 GTGAATGAGAGTGGCATCTTATTAATCTTATTTTCCACAAATATTTTGGAAAGCCAC 1668  
 Qy 621 PheAsnArgIleSerLeuLeuGly 629  
 Db 1669 TTCAATAGATTTTCACTTGGAAAAAG 1695  
 RESULT 14  
 US-09-972-708-29  
 / Sequence 29, Application US/09972708  
 / Publication No. US20030059871A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Immunex Corporation  
 / APPLICANT: Cosman, David U.  
 / APPLICANT: Mosley, Bruce A.  
 / APPLICANT: Bird, Timothy A.  
 / APPLICANT: DiBose, Robert F.  
 / APPLICANT: Wiley, Steven R.  
 / TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPR1 AND HPR2  
 / FILE REFERENCE: 3160-B  
 / CURRENT APPLICATION NUMBER: US/09/972, 708  
 / CURRENT FILING DATE: 2001-10-05  
 / NUMBER OF SEQ ID NOS: 29  
 / SOFTWARE: PatentIn version 3.1  
 / SEQ ID NO 29  
 / LENGTH: 1935  
 / TYPE: DNA  
 / ORGANISM: Mus musculus  
 / US-09-972-708-29  
 Alignment Scores:  
 Pred. No.: 5,93e-244 Length: 1935  
 Score: 2280.50 Matches: 432  
 Percent Similarity: 78.2% Conservative: 76  
 Best Local Similarity: 66.5% Mismatches: 115  
 Query Match: 68.6% Indels: 27  
 DB: 3 Gaps: 4  
 US-10-667-289-2 (1-629) x US-09-972-708-29 (1-1935)  
 Qy 1 MetAsn\*\*ValThrIleGlnTrpAspAlaValileAlaLeuTyrIleLeuPheSerTrp 20  
 Db 1 ATAGAGTCACTCACTCACTCACTGCGATGCGATGCGATGCGATGCGATGCGATGCGATG 60  
 Qy 21 CyHisGlyGlyIleThrAsnIleAsnCyseSerGlyHisIleTrpValileGluProAlaThr 40  
 Db 61 TGTCAAGAGAAATCAACAGTATTAATCTGCTGCGTGAATGCGGTTGAGCTGCTGCGAA 120  
 Qy 41 IlePheLyseMetGlyMetAsnIleSerIleTyrCyseGlnAlaAlaIleLyserAsnCyseGln 60  
 Db 121 ATTTTCAAGTGGGCAATTAATGTTTCTATATATTTGCGCAACAGCCCTTAAGCACTGCCA 180  
 Qy 61 ProArgLyserHisPheTyrLyserAsnGlyIleLyseGluArgPheGlnIleThrArgIle 80  
 Db 181 CCAAGAAATCTTACTTTATTAATAATGCTTCAAGAAATAATTTGATATCAAGAGATT 240  
 Qy 81 AsnLyserThrThrAlaArgLeuTyrTyrLyserAsnPheLeuGluProHisAlaSerMetTyr 100  
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 Qy 101 CyThrIleGluCyseProLyserHisPheGlnGluThrLeuIleCyseGlyLyserAspIleSer 120  
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Db      1 ATGAGTCACTGACACTGTCATGTGTGATGATGACCCCTTATATGCTCTTCAGATGG 60
Qy      21 CysH1sglyglyIleThrAsnIleAsnGlySerGlyHisIleThrValGluProAlaThr 40
Db      61 TGTCAAGGAAATCACAAGATTAATGCTCTGTGTGATGATGATGATGATGATGATGATGAT 120
Qy      41 IlePheLysMetGlyMetAsnIleSerIleThrCysGlnAlaAlaIleLysAsnGlyGln 60
Db      121 ATTTTCAGATGGGCAATTAATGTTTCTATATATGTCACAAAGAGCCCTTAAGCACTGCCGA 180
Qy      61 ProArgLysLeuHisPheThrLysAlaGlnGlyIleLysGlnLysPheGlnIleThrArgIle 80
Db      181 CCAAGGAATCTTATCTTTATTAATAAATGCTTCAAAAGAAATTTGATATCACAAGGATTT 240
Qy      81 AsnLysThrThrAlaArgLysLeuThrPheLysAsnLysPheGluProHisAlaSerMetThr 100
Db      241 AATGGAACAACAGCTCGATTTGATTAAGGCTTTTCGAAAGCTCAAGCTCAATGTCAT 300
Qy      101 CysThrAlaGluCysProLysHisPheGlnGlnThrLeuIleCysGlyLysAsnIleSer 120
Db      301 TGCACCTGCAATGCTCGTCAATTTCAAGAGACATGATTTGTGGGAAAGACATTTCC 360
Qy      121 SerGlyThrProProAlaIleProAspGluValThrCysValIleThrGlyThrSerGly 140
Db      361 TCTGACATCCACCGAATGCCCGGCAATCTGACATGTCATTTATGAAATCTCAGGC 420
Qy      141 AsnMetThrCysThrTPAsnAla**LysLeuThrThrIleAspThrLysValVal 160
Db      421 AACATGACATGACCTGGAACACGAGAACCTTACATCATGATACCAAGATATATTGTG 480
Qy      161 HisValLysSerLeuGlnThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 180
Db      481 CATGTGAAGAGTTGGAGACAGAAAGAAACAACAATATCTTCCTCAAGCTATGTTAAG 540
Qy      181 IleSerThrAspSerLeuGlnGlnGlyLysLysThrLeuValIleProValAlaAlaAsn 200
Db      541 ATCTCCACTACTACTACGACAGGACAGAGGATTTGTATGTGATGATGATGATGATGAT 600
Qy      201 AlaLeuGlyMetGluGluSerLysGlnLeuGlnIleHisLeuAspAspIleValIlePro 220
Db      601 TCCTTAGGCACTGAGAACTCAACAACATCAAGCTCATCTGATGATATATGATATCT 660
Qy      221 SerAlaAlaValIleSerArgAlaGluThrIleAsnAlaThrValProLysThrIleIle 240
Db      661 TCTGCGTCATCATTTCCAGGCTGAGACATCAACAACATCTGATCCCAAGACCATAGTT 720
Qy      241 TyrThrAspSerGlnThrThrIleGlnLysValSerCysGluMetArgLysValIleThr 260
Db      721 TACTGAAAAGCAAACTATGATTTGAGAAAGATTTCTGTAGATGATGATGATGATGATGAT 780
Qy      261 ThrAsnGlnThrTPAsnValLysGluPheAspThrAsnPheThrValGlnGlnSer 280
Db      781 ACAACCAAAAGCTGAGATGTTAAAGAAATTTGAGCCCAATTTCAATATGATGACGACTCA 840
Qy      281 GluPheThrLeuGluProAsnIleLysThrValPheGlnValArgCys----- 296
Db      841 GAATTCTACCTGAGCAGACAGCAAGATATGATTTCAAGTGCATGTCAAGAAACTGCT 900
Qy      297 -----GlnGlnThrGly 300
Db      901 AAAAGAACTGGCAGCCTGGAGTTCCCTTTGTGCCAACAACTTCCCAAGAAACTGGT 960
Qy      301 LysArgThrTPAsnProLysSerProPhePheHisLysThrProGlnThrValPro 320
Db      961 AAAAGAACTGGCAGCCTGGAGTTCCCTTTGTGCCAACAACTTCCCAAGAACTGGT 1020
Qy      321 GlnValThrSerLysAlaPheGlnHisAspThrTPAsnSerGlyLeuThrValAlaSer 340
Db      1021 CAGGTTACAGCAAAATCA---TCCACGAACCTCAGAAAGATGAGATGCTCAGTGTACA 1077
Qy      341 IleSerThrGlyHisLeuThrSerAspAsnArgLysAlaIleGlyLeuLeuLeuGlyMet 360
Db      1078 ATCTTCAGAGACATCTCTGCTTCAAGTATCATCAACAATGGAATTTGTGTGGGAATG 1137

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Qy      361 IleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380
Db      1138 GTCCTTCTGGCCATCATGATGTTGCCGATTTTCTCTGATTTGGATATTAACAGATCACTT 1197
Qy      381 ArgThrGlyIleLysArgAlaGlyIleLeuLeuLeuIleProLysThrPheLysValIle 400
Db      1198 CGATAGGAATTTAAAGAAAGTTTATCTGATATATCTCAAAAGTGTGCTTTATGAAAGATTT 1257
Qy      401 ProAsnMetLysAsnSerAsnValIleLysMetLeuGlnGlnLysAsnSerGluLeuMetAsn 420
Db      1258 CTTAATATGGAATAATGCAATGTTGCAAAATTTATACAGAAAAAAGTATATTTGAGAT 1317
Qy      421 AsnAsnSerSerGluGlnValIleLysValAspProMetIleThrGluIleLysGluIle 440
Db      1318 GATATGCCAGTGAAGCAGGCCCTGTATGTGATCTGTCTTACAGAGATTAAGTGAATC 1377
Qy      441 PheIleProGlnHisLysProThrAspThrLysLysGluAsn---ThrGlyProLeuGln 459
Db      1378 TCTCCCTGGAAACAACCCACAGATTCACAAAGAAAGAGCTCACAGACCTCTTGAG 1437
Qy      460 ThrArgAspThrProGlnAsnSerLeuPheAspAsnThrValValIleThrIleProAsp 479
Db      1438 ACAAGACATGCTCTCTAGGAATGTTGTCTACAGATTTCTGTGTGTATATCTTGAC 1497
Qy      480 LeuAsnThrGlyThrLysProGlnIleSerAsnPheLeuProGluLysSerHisLeuSer 499
Db      1498 CTCACACTGATATACAAACCCAGGTTTCAATGTTCTCTCGAGAGAAACCTTTTCATT 1557
Qy      500 AsnAsnAsnGluIleThrSerLeuThrLeuLysProProValAspSerLeuAspSerGly 519
Db      1558 AACAGAGATGAAAGAGACCTTACATCCCTTGAACCAACAGATACCACTT----- 1608
Qy      520 AsnAsnProArgLeuGlnLysHisProAsnPheAlaPheSerValSerSerValAsnSer 539
Db      1609 -----GCCAGATTGAAACATATCCCACTTCAATTTTCTCTCAAGATATGCTTTA 1662
Qy      540 LeuSerAsnThrIlePheLeuGlyGluLeuSerLeuIleLeuAsnGlnGlyCysSer 559
Db      1663 CTAACAAAACATATTTCTGATGATATGTCCTGTTTAATCAAGAGAAATTCAT 1722
Qy      560 SerProAspIleGlnAsnSerValGlnGlnGlnThrThreLeuLeuGluAsnAspSer 579
Db      1723 TCTCTGACATTAATAAACTCAAGACAGAGAGAAACAGCATCTTTGCAAAAGTACTCA 1782
Qy      580 ProSerGlnThrIleProGlnGlnThrLeuLeuProAspGluPheValSerCysLeuGly 599
Db      1783 CCAAGTGAACATATCCAGGCGAGACTCTGTGTCTGATGATATTTGTCTCTGTTGGCA 1842
Qy      600 IleValAsnGluLeuProSerIleAsnThrThrPheProGlnAsnIleLeuGluSer 619
Db      1843 ATGGAGATGAGACATTCATATTAATTTCACTTTCACACAGAACGTTTGGAAAGC 1902
Qy      620 HisPheAsnArgIleSerLeuLeuGluLys 639
Db      1903 CATTTCAGTGAATTTCACTTCCAAAG 1932

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Search completed: October 14, 2006, 17:25:45  
 Job time : 2007 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_p2n model

Run on: October 14, 2006, 14:43:19 | Search time 365 Seconds

(without alignments)  
4829.870 Million cell updates/sec

Title: US-10-667-289-2

Sequence: 1 MNXYTIQMDVIALYILFSW.....TYFPQNIESHFNRIISLEK 629

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2395520 seqs, 934235491 residues

Total number of hits satisfying chosen parameters: 4791040

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODE=frame\_p2n.model -DEV=x1h  
-Q=abses/ABSMBE.spool/US10667289/runat\_13102006\_111543\_24573/app\_query.fasta.1  
-DB=Published.Applications.NA.New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsu62  
-TRANS=human40.cdt -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -HOST=abses02h  
-USER=US10667289 -OCGN\_1\_1\_238 -runat\_13102006\_111543\_24573 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELop=6 -DELEXT=7

Database :

Published Applications NA.New:\*  
1: /EMC\_Celerra\_SIDS3/ProdData/1/pubpna/US09\_NEW\_PUB.seq:\*  
2: /EMC\_Celerra\_SIDS3/ProdData/1/pubpna/US06\_NEW\_PUB.seq:\*  
3: /EMC\_Celerra\_SIDS3/ProdData/1/pubpna/US07\_NEW\_PUB.seq:\*  
4: /EMC\_Celerra\_SIDS3/ProdData/1/pubpna/US08\_NEW\_PUB.seq:\*  
5: /EMC\_Celerra\_SIDS3/ProdData/1/pubpna/PCT\_NEW\_PUB.seq:\*  
6: /EMC\_Celerra\_SIDS3/ProdData/1/pubpna/US10\_NEW\_PUB.seq:\*  
7: /EMC\_Celerra\_SIDS3/ProdData/1/pubpna/US11\_NEW\_PUB.seq:\*  
8: /EMC\_Celerra\_SIDS3/ProdData/1/pubpna/US11\_NEW\_PUB.seq1:\*  
9: /EMC\_Celerra\_SIDS3/ProdData/1/pubpna/US11\_NEW\_PUB.seq2:\*  
10: /EMC\_Celerra\_SIDS3/ProdData/1/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3314	99.6	1910	8	US-11-274-375-9
2	3292	99.0	2123	8	US-11-274-375-5
3	2192	65.9	1301	8	US-11-274-375-7
4	2175	65.4	1479	8	US-11-274-375-3
5	1695	51.0	1784	8	US-11-274-375-1
6	286	8.6	360	8	US-11-274-375-23
7	216	6.5	4040	8	US-11-266-748A-32008

8	209	6.3	3085	8	US-11-266-748A-28955	Sequence 28955, A
9	203	6.1	3159	8	US-11-266-748A-31490	Sequence 31490, A
10	190	5.7	2723	8	US-11-330-726-179	Sequence 179, App
11	190	5.7	2736	6	US-10-669-920-109	Sequence 109, App
12	189	5.7	3162	8	US-11-266-748A-29132	Sequence 29132, A
13	189	5.7	1869	7	US-11-330-726-180	Sequence 180, App
14	188	5.7	5252	6	US-10-511-937-3101	Sequence 3101, App
15	188	5.7	5252	6	US-10-511-937-3102	Sequence 3102, App
16	186.5	5.6	1989	7	US-11-353-451-7	Sequence 7, Appl1
17	186.5	5.6	2199	7	US-11-353-451-5	Sequence 5, Appl1
18	186.5	5.6	2903	9	US-11-301-764-4	Sequence 4, Appl1
19	173	5.2	2295	9	US-11-301-764-38	Sequence 38, Appl1
20	170	5.1	1557	7	US-11-353-427-5	Sequence 5, Appl1
21	170	5.1	1557	9	US-11-353-454-5	Sequence 5, Appl1
22	170	5.1	1557	9	US-11-301-764-70	Sequence 70, Appl1
23	165.5	5.0	1716	8	US-11-300-928-28	Sequence 28, Appl1
24	165.5	5.0	1790	8	US-11-286-092-31	Sequence 31, Appl1
25	165.5	5.0	1790	8	US-11-286-155-31	Sequence 31, Appl1
26	165	5.0	1425	6	US-10-669-920-101	Sequence 101, App
27	163.5	4.9	2583	8	US-11-266-748A-56095	Sequence 56095, A
28	163.5	4.9	3003	6	US-10-511-937-2820	Sequence 2820, App
29	163.5	4.9	3029	8	US-11-266-748A-27795	Sequence 27795, A
30	160.5	4.8	1344	6	US-10-669-920-107	Sequence 107, App
31	157.5	4.7	1989	7	US-11-353-451-13	Sequence 13, Appl1
32	157.5	4.7	2728	9	US-11-301-764-113	Sequence 113, App
33	157.5	4.7	2748	7	US-11-353-427-7	Sequence 7, Appl1
34	157.5	4.7	2748	7	US-11-353-454-7	Sequence 7, Appl1
35	157.5	4.7	2748	9	US-11-301-764-111	Sequence 11, App
36	155.5	4.7	2356	6	US-10-669-920-94	Sequence 94, Appl1
37	153	4.6	975	7	US-11-353-451-9	Sequence 9, Appl1
38	148	4.4	1827	7	US-11-330-726-177	Sequence 177, App
39	148	4.4	1831	7	US-11-330-726-176	Sequence 176, App
40	147	4.4	720	7	US-11-353-451-11	Sequence 11, Appl1
41	140.5	4.2	4968	8	US-11-266-748A-31664	Sequence 31664, A
42	140.5	4.2	5157	8	US-11-266-748A-56701	Sequence 56701, A
43	139.5	4.2	1538	8	US-11-266-748A-250506	Sequence 250506, A
44	139.5	4.2	1538	8	US-11-266-748A-311023	Sequence 311023, A
45	139	4.2	1101	6	US-10-669-920-103	Sequence 103, App

#### ALIGNMENTS

RESULT 1  
US-11-274-375-9  
; Sequence 9, Application US/11274375  
; Publication No. US20060106201A1  
; GENERAL INFORMATION:  
; APPLICANT: Maeda, Masatugu  
; APPLICANT: Yaguchi, Noriko  
; TITLE OR INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12  
; FILE REFERENCE: 06501-105U31  
; CURRENT APPLICATION NUMBER: US/11/274,375  
; CURRENT FILING DATE: 2005-11-14  
; PRIOR APPLICATION NUMBER: US/10/105,930  
; PRIOR FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER: PCT/JP00/06654  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: JP 2000-240397  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: JP 11-273358  
; PRIOR FILING DATE: 1999-09-27  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 1910  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1887)  
; US-11-274-375-9

Alignment Scores:

Pred. No.: 3,74e-315 Length: 1910  
 Score: 3314.00 Matches: 626  
 Percent Similarity: 99.5% Conservative: 0  
 Best Local Similarity: 99.5% Mismatches: 3  
 Query Match: 99.6% Indels: 0  
 DB: 8 Gaps: 0

US-10-667-289-2 (1-629) x US-11-274-375-9 (1-1910)

QY 1 MetAsn\*\*ValThrIleGlnTrpAspAlaValIleAlaLeuTyrIleLeuPheSerTrp 20  
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 QY 21 CysHisGlyGlyIleThrAsnIleAsnCysSerGlyHisIleTrpValGluProAlaThr 40  
 Db 61 TGTCAATGAGGAATTAACAATATATTAACCTGCTGGCCACATCTGGTGAACAAGCCACA 120  
 QY 41 IlePheLeuMetGlyMetAsnIleSerIleTyrCysGlnAlaAlaIleValAsnCysGln 60  
 Db 121 ATTTTAAAGATGGGTAAATATCTATATATATGCGAAGCAAGCAATTAAGAACTGCCAA 180  
 QY 61 ProArgLeuHisPheTyrLysAsnGlyIleLysGluArgPheGlnIleThrArgIle 80  
 Db 181 CCAAGGAACTTCCTTTTATTAATAATGGCATCAAGAAAGATTTCAAAATCACAGGAAT 240  
 QY 81 AsnLysThrThrAlaArgLeuTrpTyrLysAsnPheLeuGluProHisAlaSerMetTyr 100  
 Db 241 AATTAACAACAGCTCGGCTTGGTATTAATACTTCGGAACACATGCTTCTATGTAC 300  
 QY 101 CysThrIleGluCysProLysHisPheGlnGluThrLeuIleCysGlyLysAsnIleSer 120  
 Db 301 TGCACTCTGATATCCCAACATTTTCAAGACACCTGATATGTGAAGAAAGACATTTCT 360  
 QY 121 SerGlyTyrProAspIleProAspGluValThrCysValIleTyrGluTyrSerGly 140  
 Db 361 TCTGGATATCCGCCAGATATCTCGATGAAGTAACTGTGCATTTATGAATATATTCAGCC 420  
 QY 141 AsnMetThrCysThrTrpAsnAla\*\*LysLeuThrTyrIleAspThrLysTyrValVal 160  
 Db 421 AACATGACTTGCACTGGAATGCTGGAAAGCTCACTACATAGACAAATAATGTGGTA 480  
 QY 161 HisValLysSerLeuGluThrGluGluGluGlnIleThrLeuThrSerSerTyrIleAsn 180  
 Db 481 CATGTGAAGAGTTTGAAGACGAAGAAAGACACAGATCTCACTCAAGCTAATATTAAC 540  
 QY 181 IleSerThrAspSerLeuGlnGlyLysLysTyrLeuValTrpValGlnAlaAsn 200  
 Db 541 ATCTCCACTGATTTATTAACAAGGTGGCAAGAAAGTCTGGTTGGTCCAAAGCCAAAC 600  
 QY 201 AlaLeuGlyMetGluGluSerLysGlnLeuGlnIleHisLeuAspAspIleValIlePro 220  
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 QY 221 SerIleAlaValIleSerIleGluThrIleAsnAlaThrValProLysThrIleIle 240  
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 QY 241 TyrTrpAspSerGlnThrThrIleGluLysValSerCysGluMetArgTyrLysAlaThr 260  
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 Db 841 GAATTTCACTGAGCCAAACATTAAGTACGTATTTTCAAGTGAAGATGCAAGAAACAGGC 900  
 QY 301 LysArgTyrTrpGlnProTrpSerSerProPhePheHisLysThrProGluThrValPro 320  
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QY 321 GluValThrSerLysAlaPheGlnHisAspThrTrpAsnSerGlyLeuThrValAlaSer 340  
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 Db 1201 CCTAATATGAAACAGCAATGTTGTGAATACTACAGAAATATGTAACCTTAATGAAT 1260  
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 QY 441 PheIleProGluHisLysProThrAspTyrLysArgLysAsnThrGlyProLeuGluThr 460  
 Db 1321 TTCACTCCCAACACAAAGCCTTACAGACTTCAAAAGAGAAATACAGAGCCCTGGAGACA 1380  
 QY 461 ArgAspTyrProGluAsnSerLeuPheAspAsnThrThrValValTyrIleProAspLeu 480  
 Db 1381 AGAGACTACCCGCAAACTGCTATTTGCAACATACATCAAGTTTATATATCTGATCTC 1440  
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 Db 1561 AATCCAGATTACAAAGCATCTTAATTTTGTCTTTTCTGTTTCAAGTGGAAATTCATTA 1620  
 QY 541 SerAsnThrIlePheLeuGlyGluLeuSerLeuIleLeuAsnGlnGlyCysSerSer 560  
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 QY 561 ProAspIleGlnAsnSerValGluGluGluThrThrMetLeuLeuGluAsnAspSerPro 580  
 Db 1681 CTTGACATTAACAAACTCAAGTGAAGAGAAACCACTGCTTTTGGAAATGATTCACCC 1740  
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 Db 1741 AGTGAACATAATCCAGAAACAGACCTGCTCTCTGATGAATTTGTCTCTTGGGGATC 1800  
 QY 601 ValAsnGluLysLeuProSerIleAsnThrTyrPheProGluAsnIleLeuGluSerHis 620  
 Db 1801 GTGAATAGAGAGTTGCCATATTAATTAATCTTATTTTCAAAAATATTTTGGAAAGCAC 1860  
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 Db 1861 TTCAATAGATTTCACTCTTGAAAAAG 1887

# RESULT 2

US-11-274-375-5

; Sequence 5, Application US/11274375

; Publication No. US20060106201A1

; GENERAL INFORMATION:

; APPLICANT: Meeda, Maatsugu

; APPLICANT: Yasuchi, Noriko

; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12

; FILE REFERENCE: 06501-105US1



CURRENT APPLICATION NUMBER: US/11/274,375  
CURRENT FILING DATE: 2005-11-14  
PRIOR APPLICATION NUMBER: US/10/105,930  
PRIOR FILING DATE: 2002-03-25  
PRIOR APPLICATION NUMBER: PCT/JP00/06654  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: JP 2000-240397  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: JP 11-273358  
PRIOR FILING DATE: 1999-09-27  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5  
LENGTH: 2123  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (98) ... (1984)  
US-11-274-375-5

Alignment Scores:  
Pred. No.: 6,276-313 Length: 2123  
Score: 3292.00 Matches: 622  
Percent Similarity: 99.2% Conservative: 2  
Best Local Similarity: 99.0% Mismatches: 5  
Query Match: 99.0% Indels: 0  
DB: Gaps: 0

US-10-667-289-2 (1-629) x US-11-274-375-5 (1-2123)

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Qy 21 CysHisGlyGlyIleThrAsnIleAsnGlySerGlyHisIleTrpValGluProAlaThr 40  
Db 158 TGTGATGAGGAATTAACAATATAAATGCTGCGCCACATCTGGTGAAGACGACCA 217  
Qy 41 IlePheLeuMetGlyMetAsnIleSerIleTyrCysGlnAlaAlaIleValAsnGlyGln 60  
Db 218 ATTTTAAAGATGGGTGGAATATCTCTATATATTGCCAAGACGCAATTAAGAACTGCCAA 277  
Qy 61 ProArgLeuHisPheTyrIleAsnGlyIleLeuGluArgPheGlnIleThrArgIle 80  
Db 278 CCAAGGAATCTTCAATTTTAAATAATGCAATCAAGAAAGATTCAAAATCAAGAAAT 337  
Qy 81 AsnLeuThrAlaAlaGluLeuTyrIleAsnPheLeuGluProHisAlaSerMetTyr 100  
Db 338 AATTAACAACAGCTCGCTTGGTATTAATAAATCTTCTGGAACACATGCTTCTATGTC 397  
Qy 101 CysThrAlaGluCysProLeuHisPheGlnGluThrIleIleCysGlyValAspIleSer 120  
Db 398 TGCACTGCTCAATGCTCCAAACATTTTCAAGAGACATGATATGGAAGAAACATTTCT 457  
Qy 121 SerGlyTyrProProAspIleProAspGluValThrCysValIleTyrGluTyrSerGly 140  
Db 458 TCTGGATATCCGCGCATATCTCTGATGAAGTAACCTGTGATTAAGATATTCAGGC 517  
Qy 141 AsnMetThrCysThrIleAsnAla\*\*LysLeuThrTyrIleAspThrIleValVal 160  
Db 518 AACATGACTTGACCTGGAAATGCTGAGGCTCACATACATAGACAAATAATGCTGTA 577  
Qy 161 HisValLysSerLeuGluThrGluGluGluGluGluGluGluGluGluGluGluGlu 180  
Db 578 CATGTGAAGAGTTTGAAGACAGAAAGACAGACAGATCTCACTCAAGCTATATTAAC 637  
Qy 181 IleSerThrAspSerLeuGluGlyLysLeuTyrIleValIleValGlnAlaAsn 200  
Db 638 ATCTCCCTGATTCATTAACAGGTGGCAAGAGTACTTGGTTGGGTCCAGACGCAAC 697  
Qy 201 AlaLeuGlyMetGluSerLysGluLeuGlnIleHisLeuAspAspIleValIlePro 220

Db 698 GCACTAGGATGAGAGATGCAAAACATGCAAAATTCACCTGATGATATAGTACTT 757  
Qy 221 SerAlaIleValIleSerArgAlaGluThrIleAsnAlaThrValProLysThrIleIle 240  
Db 758 TCTGACCCGCTCATTTCCAGGGCTGAGACTATTAATCTTACAGTCCCAAGACATTAAT 817  
Qy 241 TyrTrpAspSerGlnThrIleGluLysValSerCysGluMetArgTyrLysAlaThr 260  
Db 818 TATTTGGATAGTCAACCAACATTTGAAGAGTTTCTGTAATATGATACCAAGCTACA 877  
Qy 261 ThrAsnGlnThrIleAsnValLysGluPheAspThrAsnPheThrTyrValGlnIleSer 280  
Db 878 ACAACCAACCTTGATGTTAAAGATTGACCACTTAATTTATATATGTCACACATGCA 937  
Qy 281 GluPheTyrLeuGluProAsnIleLysTyrValPheGlnValArgGluGlnIleThrGly 300  
Db 938 GAATTCATCTTGAGCCAAACATTAAGTATGATTCAGTGAATGATTCAGAAACAGGC 997  
Qy 301 LysArgTyrTrpGluProTrpSerSerProPhePheHisLysThrProGluThrValPro 320  
Db 998 AAAAGTACTGGCAGCTTGGAGTTCCTGTTTTTCAATAAACACCTGAACAGTTCCC 1057  
Qy 321 GlnValThrSerLysAlaPheGlnHisAspThrTrpAsnSerGlyLeuThrValAlaSer 340  
Db 1058 CAGGTCAATCAAAAGCATTCACATGACACATGGAATTCGGGCTTAACAGTTGCTTCC 1117  
Qy 341 IleSerThrGlyHisLeuThrSerAspAsnArgLysAspIleGlyLeuLeuLeuGlyMet 360  
Db 1118 ATCTTCAAGGGACCTTACTTCTGACACAGAGACATTTGACTTTATTTGGAAATG 1177  
Qy 361 IleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380  
Db 1178 ATGCTCTTCTGTTATGTTGTCAATCTTCTTGAATGGACATTTACAGATCAATTC 1237  
Qy 381 ArgThrGlyIleLysArgArgIleLeuLeuLeuIleProLysTrpLeuTyrGluAspIle 400  
Db 1238 CGAATCGGATTAAGAAAGATCTTATGTTATATCAAAAGTGGCTTTATGAAGATATT 1297  
Qy 401 ProAsnMetLysAsnSerAsnValLysLeuLeuGlnLysAsnSerGluMetAsn 420  
Db 1298 CCTAATATGAAAACAGCAATGTTGTAATAATCTACAGAAATATGAACTTATATAT 1357  
Qy 421 AsnAsnSerSerGluGlnValLeuTyrValAspProMetIleThrGluIleLysGluIle 440  
Db 1358 AATTAATCCAGTGAAGAGGCTCTATATGTTGATCCCATGATTAACAGAGATTAAGAAATC 1417  
Qy 441 PheIleProGluHisLysProThrAspTyrLysLeuGluAsnThrGlyProLeuGluThr 460  
Db 1418 TTCATCCAGAAACAAAGCCTTACAGACTACAAAGAGAGAAATACAGGACCCCTGAGACA 1477  
Qy 461 ArgAspTyrProGluAsnSerLeuPheAspAsnThrThrValValTyrIleProAspLeu 480  
Db 1478 AGAGACTACCCGCAAAACCTGCTATTCGACAAATACACATTTGATATATATCTCGAATTC 1537  
Qy 481 AsnThrGlyTyrLysProGlnIleSerAsnPheLeuProGluGlySerHisLeuSerAsn 500  
Db 1538 AACACTGGAATTAACCCCAATTTCAATTTCTGCTGAGGAGAACCATCTCAAGTAAT 1597  
Qy 501 AsnAsnGluIleThrSerLeuThrLeuLysProProValAspSerLeuAspSerGlyAsn 520  
Db 1598 AATTAATGAATTAATCTTCACTTAACATTAACCAACAGTTGATTCCTTAAGACTCAGGAAT 1657  
Qy 521 AsnProArgLeuGlnLysHisProAsnPheAlaPheSerValSerSerValAsnSerLeu 540  
Db 1658 AATCCCAAGTTACAAAGACATCTTAATTTGCTTTTCTGTTTCAGATGGAATTCACIA 1717  
Qy 541 SerAsnThrIlePheLeuGluGluLeuSerLeuIleLeuAsnGlnGlyCysSerSer 560  
Db 1718 AGCAACACATATTTCTTGGAGAAATTAAGCTCATATTAATCAAGAGAAATCAAGTTCT 1777  
Qy 561 ProAspIleGlnAsnSerValGluGluGluThrThrMetLeuLeuGluLysAsnAspSerPro 580  
Db 1778 CCTGACATACAAATCTAGTATGAGAGAAACCAACCATGCTTTTGGAAATGATTCACCC 1837

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Qy 581 SerGluThrIleProGluGlnThrLeuLeuProAspGluPheValSerCysLeuGlyIle 600
Db 1638 AGTGAACATTCCTCCAGAACAGACCCCTCTCCGATGAAATTTGCTCTCTGTTGGGATC 1697
Qy 601 ValAsnGluGluLeuProSerIleAsnThrTyrPheProGlnAsnIleLeuGluSerHis 620
Db 1898 GTGATATGAGATGGTCCATCATTAATACTAATTTCCACAAATATTTGGAAAGCCAC 1957
Qy 621 PheAsnArgIleSerLeuLeuGluLys 629
Db 1958 TTCAATAGAAATTCATCTTGAAAAAG 1984

RESULT 3
US-11-274-375-7
; Sequence 7, Application US/11274375
; Publication No. US20060106201A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; APPLICANT: Yasuchi, Noriko
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105US1
; CURRENT APPLICATION NUMBER: US/11/274,375
; PRIOR FILING DATE: 2005-11-14
; PRIOR APPLICATION NUMBER: US/10/105,930
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: PCT/JP00/06654
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: JP 2000-240397
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP 11-273358
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1301
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1284)
; US-11-274-375-7

Alignment Scores:
Pred. No.: 3e-205 Length: 1301
Score: 2192.00 Matches: 410
Percent Similarity: 99.3% Conservative: 0
Best Local Similarity: 99.3% Mismatches: 3
Query Match: 65.9% Indels: 0
DB: Gaps: 0

US-10-667-289-2 (1-629) x US-11-274-375-7 (1-1301)
Qy 1 MetAsn***ValThrIleGlnThrAspAlaValIleAlaLeuTyrIleLeuPheSerTyr 20
Db 1 ATGATATCAGGTCACATTCATTCATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 60
Qy 21 CysHisGlyGlyIleThrAsnIleAsnCysSerGlyHisIleTyrPheValGluProAlaThr 40
Db 61 TGTATGAGAGAAATTTACAAATATAACTGCTGCGCCACATCTGGATGAGAACGACGCA 120
Qy 41 IlePheLysMetGlyMetAsnIleSerIleTyrCysGlnAlaAlaIleLysAsnCysGln 60
Db 121 ATTTTAAAGATGGGTATGAAATATCTCTATATATGGCAAGACGAAATTAAGAACTGGCAA 180
Qy 61 ProArgLysLeuHisPheTyrLysAsnGlyIleLysGluArgPheGlnIleThrArgIle 80
Db 181 CCAAGGAAACTTCAATTTTATATAAAATGCGCATCAAGAAAGATTTCAATATCAAGGATTT 240
Qy 81 AsnLysThrThrAlaArgLeuTyrTyrLysAsnPheLeuGluProHisAlaSerMetTyr 100
Db 241 AATAAAACAACAGCTCGGCTTGTGATATAAAATTTCTGGAACACAGCTTCTATGTAC 300
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Qy 101 CysThrAlaGluCysProLysHisPheGlnGluThrLeuIleCysGlyLysAspIleSer 120
Db 301 TGCATCTGTAATGTCCTCCAAACATTTTCAAGAGACACTGATATGTGAAAAAGCATTTCT 360
Qy 121 SerGlyTyrProProAspIleProAspGluValIleThrCysValIleTyrGlyTyrSerGly 140
Db 361 TCTGATATCCGCAATATCTCTGATGAAAGTAACTGTCTATTAATGAAATTTCAAGGC 420
Qy 141 AsnMetThrCysThrTrpAsnAla***LysLeuThrTyrIleAspThrLysTyrValIle 160
Db 421 AACATGACTTGACACCTGGAATGCTGGGAAGCTCACTACATACACAAATAACGTGGTA 480
Qy 161 HisValLysSerLeuGluThrGluGluGlnGlnThrLeuThrSerSerTyrIleAsn 180
Db 481 CATGTGAAGATTTAGAGACAGAAAGAGCAACAGATCTCACCTCAAGCTATATTAAAC 540
Qy 181 IleSerThrAspSerLeuGlnGlyLysLysTyrLeuValTrpValGlnAlaAlaAsn 200
Db 541 ATCTCCACGTATTCATTAACAGGTGGCAGAGTACTGTGGTTCAGGTCACAGACGAAAC 600
Qy 201 AlaLeuGlyMetGluGluSerLysGlnLeuGlnIleHisLeuAspAspIleValIlePro 220
Db 601 GCATGAGCATGGAAGATGAAAGTAAACAACAGTCAATTCACCTGATATAGTATGATACCT 660
Qy 221 SerAlaAlaValIleSerArgAlaGluThrIleAsnAlaThrValProLysThrIleIle 240
Db 661 TCTGCAAGCCGTCATTTCCAGGGCTGAGACTATTAATGCTACAGTGCACCAAGCATTAAT 720
Qy 241 TyrTrpAspSerGlnThrThrIleGluLysValSerCysGluLysArgTyrLysAlaThr 260
Db 721 TATTTGATATGTAACAAACAAATTTGAAGGTTTCCTGTAAATGAGATCAAGGCTACA 780
Qy 261 ThrAsnGlnThrTrpAsnValLysGluPheAspThrAsnPheThrTyrValGlnGlnSer 280
Db 781 ACAACCAACCTTGAAATGTTAAAGAAATTTGACACCAATTTTACATATGTGCAACGTCA 840
Qy 281 GluPheTyrLeuGluProAsnIleLysTyrValPheGlnValArgCysGlnGluThrGly 300
Db 841 GAATTCATCTGAGGCCAAACATTAAGTACGATTTTCAAGTGAAGATGTCAGAAACAGGC 900
Qy 301 LysArgTyrTrpGlnProTyrPheSerProPhePheHisLysThrProGluThrValPro 320
Db 901 AAAAGGACTGGGACCTTGAGGTCACTGTTTTCATTAACACCTGAAACAGTTCCC 960
Qy 321 GlnValThrSerLysAlaPheGlnHisAspThrTrpAsnSerGlyLeuThrValAlaSer 340
Db 961 CAGTGCATCAAAAGATTCCAACATGACACATGGAATTTCTGGGCTAAACAGTTGCTTC 1020
Qy 341 IleSerThrGlyHisLeuThrSerAspAsnArgGlyAspIleGlyLeuLeuLeuGlyMet 360
Db 1021 ATCTCTACAGGACCTTACTCTTGACACACAGAGAGACATTTGACCTTTTATTTGGGAATG 1080
Qy 361 IleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380
Db 1081 ATGCTCTTCTGTTATGTTGTTCAATTTCTTTGATTTGGAATTTTAAACAATCATTC 1140
Qy 381 ArgThrGlyIleLysArgArgIleLeuLeuLeuIleProLysTrpLeuTyrGluAspIle 400
Db 1141 CGAATCGGATTTAAAGAAAGATCTTATTTGTTAATCCAAAGTGGCTTTATGAAGATTT 1200
Qy 401 ProAsnMetLysAsnSerAsnValValLysMetLeuGln 413
Db 1201 CTTAATATGAAAAACAGCATGTTGTGAAAAATGCTACAG 1239

RESULT 4
US-11-274-375-3
; Sequence 3, Application US/11274375
; Publication No. US20060106201A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; APPLICANT: Yasuchi, Noriko
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105US1
```



Pred. No.: 2.9e-156 Length: 1784  
 Score: 1695.00 Matches: 312  
 Percent Similarity: 98.7% Conservative: 2  
 Best Local Similarity: 98.1% Mismatches: 4  
 Query Match: 51.0% Indels: 0  
 DB: 8 Gaps: 0

US-10-667-289-2 (1-629) x US-11-274-375-1 (1-1784)  
 QY 1 MetAen\*\*ValThrIleGlnTrpAspAlaValIleAlaLeuTyrlleLeuPheSerTrp 20  
 Db ATGATACAGGCTACTATTTCATATGAGATGAGATATAGCCCTTTACATACCTTCAGCTGG 157  
 QY 21 CyEHISGLYLYIleThrAenIleAenCySerGlyMhiIleTyPValGluProAlaThr 40  
 Db TGTGATGAGGAATTAACAATATATACTGCTGCGCACATCTGGTGAACGACGACA 217  
 QY 41 IllePheLeuMetGlyMetAenIleSerIleTyrcyGlnIleAlaIleValAenCyGln 60  
 Db ATTTTAAAGAGGGTGAATATCTATATATGCGAAGCAGCAATTAAGAACTGCGCAA 277  
 QY 61 ProArgIleLeuHISpHeTyrlYLeaAnglyIleIleGluArgPheGlnIleThrArgIle 80  
 Db CCAAGAAACTTCTATTATTAATAATGGCATCAAGAAAGATTCAATATCAAGAGATT 337  
 QY 81 AenIleThrThrAlaArgLeuTrpTyrlYLeaAenPheLeuGluProHISAlaSerMetTyrl 100  
 Db AATTAACAACAGCTCGCTTGGTATTAATAAACTTTCGAAACGACATGCTTCTATGTAC 397  
 QY 101 CyEThrIleGluCySProLYleHISpHeGlnIleLeuIleCySerGlyLeaAspIleSer 120  
 Db TGCACTGCTGAATCTCCAAACATTTTCAGAGACATGATATGGAAGAAAGACATTCT 457  
 QY 121 SerGlyTyrlProAspIleProAspGluValThrCyValIleTyrgluTyrlSerGly 140  
 Db TCTGATATCGCGCAGATATCTCGATGAAGTATACCTGTGCATTATTAATTCAGGC 517  
 QY 141 AenMetThrCySthrTrpAenAla\*\*LYleLeuThrTyrlleAspThrIleValVal 160  
 Db AACCTGACTGACCTGAATGCTGAGAGCTCACATCAATAGACAAATATAGTGTA 577  
 QY 161 HISValIleSerLeuGluIleGluGluGluGluGluIleLeuTrpSerSerTyrlleAen 180  
 Db CATGTGAAGAGTTTGAAGACAGAAAGAGAGCAAGATCTCACCTCAAGCTATATTAAC 637  
 QY 181 IlleSerThrAspSerLeuGlnGlyLYleSerTyrlleuValTrpValGlnAlaAen 200  
 Db ATCTCCACTGATTCATTATCAAGGTGCGAAGAGTACTTGGTTGGTCCAAAGCAGCAAC 697  
 QY 201 AlaLeuGlyMetGluGluSerLYleGluGlnIleHISleuAspAspIleValIlePro 220  
 Db GCACCTAGGCAATGAAAGATCAAAACCTGCAAACTGCACTGATATATGATACTT 757  
 QY 221 SerIleAlaValIleSerArgAlaGluThrIleAenAlaThrValProLYleThrIleIle 240  
 Db TCTCAGCGCATTTCCAGGAGCTGAGACTATATATGCTACAGGCCCAACCACTAAT 817  
 QY 241 TyrlTrpAspSerGlnThrIleGluLYleValSerCyGluMetArgTyrlYLeaAlaThr 260  
 Db TATTGGATAGTCAACAACAATTGAAGAGTTCTCTGTGAATAGATTAACAAGCTACA 877  
 QY 261 ThrAenGlnThrTrpAenValLYleGluPheAspThrAenPheThrTyrlValGlnIleSer 280  
 Db ACAACACAAACTTGAAATGTTAAAGAAATTTGACACCAATTTTATCATATGTGCAACAGTCA 937  
 QY 281 GluPheTyrlleuGluProAenIleLYleTyrlValIleGlnValArgCyGlnGluIleThrGly 300  
 Db GAATTCATCTTGAGCCAAACATTAAGTACTATTTCAAGTGAATGTCAAGAAACAGGC 997  
 QY 301 LYleArgTyrlTrpGlnProTrpSerSerProPhePheHISLYleThrProGluThr 318  
 Db AAAAGGTACTGCGAGCTTGAGTTCACTGTTTTCATATAAACAACCTGAACA 1051

RESULT 6  
 US-11-274-375-23  
 ; Sequence 23, Application US/11274375  
 ; Publication No. US20060106201A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Maeda, Masatsugu  
 ; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12  
 ; FILE REFERENCE: 06501-105U51  
 ; CURRENT APPLICATION NUMBER: US/11/274,375  
 ; PRIOR FILING DATE: 2005-11-14  
 ; PRIOR APPLICATION NUMBER: US/10/105,930  
 ; PRIOR FILING DATE: 2002-03-25  
 ; PRIOR APPLICATION NUMBER: PCT/JP00/06654  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: JP 2000-240397  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: JP 11-273358  
 ; PRIOR FILING DATE: 1999-09-27  
 ; NUMBER OF SEQ ID NOS: 77  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 23  
 ; LENGTH: 360  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (140)...(295)  
 US-11-274-375-23

Alignment Scores:  
 Pred. No.: 6.1e-19 Length: 360  
 Score: 286.00 Matches: 51  
 Percent Similarity: 98.1% Conservative: 0  
 Best Local Similarity: 98.1% Mismatches: 1  
 Query Match: 8.6% Indels: 0  
 DB: 8 Gaps: 0

US-10-667-289-2 (1-629) x US-11-274-375-23 (1-360)  
 QY 267 ValIleGluPheAspThrAenPheThrTyrlValIleGlnIleSerGluPheTyrlleuGluPro 286  
 Db GTTAAAGATTTTGAACCAATTTTACATATGTGCAACAGCAAGATTTCTAGAGCCA 199  
 QY 287 AenIleSerTyrlValPheGlnValArgCyGlnGluIleThrGlyLYleArgTyrlPro 306  
 Db AACATTAAGTACGATTTCAAGTGAATGTCAAGAAACAGCAAAAGTACTGAGCCT 259  
 QY 307 TrpSerSerProPhePheHISLYleThrProGluThr 318  
 Db TGGAGTCACTGTTTTCATATAAACAACCTGAACA 295

RESULT 7  
 US-11-266-748A-33208  
 ; Sequence 32008, Application US/11266748A  
 ; Publication No. US20060134663A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Harkin, Paul  
 ; APPLICANT: Johnson, Patrick  
 ; APPLICANT: Mulligan, Karl  
 ; TITLE OF INVENTION: Transcriptome Microarray Technology and  
 ; FILE REFERENCE: 55815-0102 (319189)  
 ; CURRENT APPLICATION NUMBER: US/11/266,748A  
 ; CURRENT FILING DATE: 2005-11-03  
 ; PRIOR APPLICATION NUMBER: EP 04105479.2  
 ; PRIOR FILING DATE: 2004-11-03  
 ; PRIOR APPLICATION NUMBER: EP 04105482.6  
 ; PRIOR FILING DATE: 2004-11-03  
 ; PRIOR APPLICATION NUMBER: EP 04105483.4  
 ; PRIOR FILING DATE: 2004-11-03  
 ; PRIOR APPLICATION NUMBER: EP 04105507.0  
 ; PRIOR FILING DATE: 2004-11-03

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; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32008
; LENGTH: 4040
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-32008

Alignment Scores:
Pred. No.: 1,44e-10 Length: 4040
Score: 216.00 Matches: 75
Percent Similarity: 41.6% Conservative: 57
Best Local Similarity: 23.7% Mismatches: 131
Query Match: 6.5% Indels: 54
DB: Gaps: 13

US-10-667-289-2 (1-629) x US-11-266-748A-32008 (1-4040)
QY 32 G|H|s|l|e|t|p|v|a|l|g|u|p|r|o|l|a|t|h|r|i|e|p|h|e|y|s|e|t|g|y|m|e|t|a|n|i|e|s|e|r|i|e|t|y|r 51
DB 731 GGGCATGTGACTGGAGACCTTCACCAAGTATTTACTTGATCCACTGCATCAATATTACA 790
QY 52 C|y|e|g|i|n|a|l|a|l|e|y|s|a|n|c|y|e|g|i|n|p|r|o|a|r|g|l|y|s|e|h|i|s|h|e|t|y|r|y|s|a|n|g|i|y|l|e 71
DB 791 TGC-----TCTTGAAGCCGAGA----- 808
QY 72 L|y|e|g|i|u|a|r|p|h|e|g|i|n|l|e|h|r|a|r|g|i|e|a|n|l|y|e|h|r|t|h|r|a|a|r|g|l|e|u|t|r|y|r|y|s| 90
DB 809 CAAGCGCTTTCACCTATTCAGACGTAACAAGTTA-----ATCCTGTACAAAGTTT 859
QY 91 -----Ae|p|h|e|l|e|u|g|i|u|p|r|o|h|i|a|l|a----- 97
DB 860 GACAGAGAATTCATTTTACCATGCGCCTCCTCAATTCCTCAAGTACAGAGCTTCCC 919
QY 98 -----S|e|r|m|e|t|y|r|y|s|e|h|r|a|l|g|i|u|c|y|p|r|o|l|y|h|i|s|h|e|g|i|n|g|i|u|t|h|r|e|u 113
DB 920 CTTGGTACAACTTTGTTGTTGCTGAACTGGCTGT---ATCAATAGATGATGAATTCAA 976
QY 114 I|l|e|c|y|e|g|i|y|u|s|a|p|i|l|e|s|e|r|g|i|y|r|p|r|o|p|r|a|s|i|l|e|p|r|o|a|g|i|u|a|l|t|h|r|c|y|s 133
DB 977 ATATGTGACAGAGATCTTGTTGGTGTGCTCAGAAAGCCTCAAAATTTATCTGTC 1036
QY 134 V|a|i|l|e|t|r|o|l|u|t|r|s|e|r|g|i|y|a|n|m|e|t|h|c|y|h|r|t|h|r|a|n|a|l|a|**L|y|s|e|h|r|t|h|r|c|y|s 153
DB 1037 ATACAGAGAGAGAAACGAGGAGCTGCGCTGCACCTGGAGAGAGACGACACCCAC 1096
QY 154 I|l|e|a|s|p|h|r|t|r|y|r|v|a|l|a|l|h|i|s|e|v|a|l|-----L|y|s|e|r|l|e|u|g|i|u|t|h|r|g|i|u|g|i|u 170
DB 1097 TTTATACCTAGGTHACTCTACAGCTAAGTGACCAAAAATTTTAACTGGCAGAGCAA 1156
QY 171 G|l|n|g|i|n|t|r|e|h|r|s|e|r|t|y|r|-----I|l|e|a|n|i|l|e|s|e|r|h|t|h|r|a|s|p|s|e|r|l|e|u 186
DB 1157 TGTAAAGACATTTATTTGATTTGATTTGACCTTGAGATCAACCTCACCCGATTCACCT 1216
QY 187 G|l|n|g|i|y|u|s|y|r|l|e|u|v|a|l|t|r|p|v|a|l|a|l|a|a|n|a|l|e|u|g|i|u|c|y|m|e|t|g|i|u|g|i|u 206
DB 1217 GAA-----TCCAAATTTACAGCCAGCTTACTCTGTCAATAGCTCTTGAAGCTCTCT 1270
QY 207 S|e|r|l|e|u|g|i|n|l|e|h|i|s|e|u|a|s|p|i|l|e|v|a|i|l|e|p|r|o|s|e|r|a|i|a|l|a|v|i|l|l|e|s|e|r 226
DB 1271 TCACTTCATCCACATTCACATTTCTTGACATAGTAGGCTCTCTCTCCGAGGACAT 1330
QY 227 A|r|g|a|l|g|i|u|t|h|r|i|l|e|a|n|a|t|h|r|v|a|l|p|r|o|l|y|h|r|i|l|e|t|r|y|r|p|a|s|e|r|g|i|n|t|h|r 246
DB 1331 AGATCAAAATTTCAAAGCTTCGCTGAGAGATGATACCTTTATTTGAGAGATGAGGA 1390

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QY 247 T|h|r|i|e|g|i|u|y|e|v|a|l|s|e|r|c|y|s|g|i|u|e|c|a|r|g|t|r|y|s|a|l|a|t|h|r|t|h|r|a|n|g|i|n|t|h|r|t|r|p|a|n 266
DB 1391 CTGGTA-----CTGCTTATTCAGCTCAGATATCGCCGAGTAAACAGACAGCTCTGGAT 1444
QY 267 V|a|i|l|e|g|i|u|p|h|e|a|p|h|r|a|n|p|h|e|h|r|t|h|r|v|a|l|-----G|l|n|g|i|n|s|e|r|g|i|u|p|h|e|r|l|e|u 284
DB 1445 ATG-----GTTAATGTTCACAAAGCCAAAGAGACATGATTTGCTGGATCTG 1492
QY 285 G|l|u|p|r|o|a|n|i|l|e|y|r|t|r|v|a|l|p|h|e|g|i|n|v|a|l|a|r|c|y|e|g|i|n|-----G|u|t|h|r|g|i|y|s|a|r|g|t|y|r 303
DB 1493 AAACCAATTACAGAAATTTGAATTTTCAGATTTCTCTTAACTGATCTTTTATTAAGGAAGT 1552
QY 304 T|r|p|g|i|n|p|r|o|t|r|p|s|e|r|p|r|o|h|e|h|i|e|l|y|h|e|h|r|t|h|r|p|r|o|g|i|u|t|h|r|v|a|l|p|r|o 320
DB 1553 TGGAGTCATTTGAGTGAATTCATTTGAGAGCACAAACCCAAAGAGAGCTT 1603

RESULT 8
US-11-266-748A-28955
; Sequence 28955, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Molligan, Karl
; TITLE OR INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266, 748A
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28955
; LENGTH: 3085
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-28955

Alignment Scores:
Pred. No.: 4,78e-10 Length: 3085
Score: 209.00 Matches: 172
Percent Similarity: 32.7% Conservative: 118
Best Local Similarity: 19.4% Mismatches: 276
Query Match: 6.3% Indels: 320
DB: Gaps: 44

US-10-667-289-2 (1-629) x US-11-266-748A-28955 (1-3085)
QY 4 V|a|i|t|h|r|i|e|g|i|n|t|r|p|r|a|l|a|v|i|l|e|a|i|l|e|u|t|r|i|l|e|u|h|p|h|e|r|t|r|c|y|h|i|g|i|y 23
DB 259 TTAGCGTTGACAGCTTGGAGTGAAGCTTGTATTTCTTCTCAACCTGATGTACA 318
QY 24 G|l|y|i|l|e|h|r|a|n|i|l|e|a|n|c|y|s|e|r|g|i|y|h|i|s|l|e|t|r|p|v|a|l|g|i|u|p|r|o|l|a|t|h|r|i|l|e|h|e|y 43
DB 319 GGTGAACCTTACATCCATCT--GGTTATATCAAGTCCGTA--TCTCCAGTTGTACA 372
QY 44 M|e|c|i|y|m|e|t|a|n|i|l|e|s|e|r|i|e|t|y|r|c|y|s|g|i|n|a|l|a|i|l|e|y|s|a|n|c|y|s|i|n|p|r|o|a|r|g|l|y|s 63

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Db 373 CTTCATTTCTATATTCACGCGAGTTTGT-----GTGCTAAAGAAAAATGATGATAT 426  
Qy LeuHisPheTyrLysAsnGlyLe-----LyseGlu 73  
Db 427 TTTCATGTAAATGCTTAATTCATTTGTCTGAAAAACAACATTTTACTATTCCTTACGAG 486  
Qy ArgPheGlnIleThrArgIleAsnLysThrAlaArgLeuTyrLysAsnPheLeu 93  
Db 487 CAATATATCTATC-----ATTAACAGAAACGATCCAGTGTCACTTACCTTACGATATAGCT 540  
Qy GluProHisAlaSerMetTyrCysThrAlaGluCysProLysHisPheGlnGluThrLeu 113  
Db 541 TCATTAATATTCAGCTTCACCTTCGACACATTCCTTACCTGACAGCTTGAAACGAAT--- 597  
Qy IleCysGlyLysAspIleSerSerGlyTyrProPheAspIleProAspGluValThrCys 133  
Db 598 GTTATATGAATCACAATTAATTCAGGCTTGCTCCAGAAAAACCTTAAAAATTTGAGATTGC 657  
Qy ValIleTyrGluTyrSerGlyAsnMetThrCysThrTyrAsnAla\*\*LysLeuThrTyr 153  
Db 658 ATTGTGACGAG---GGGAAGAAAAATGAGGTGAGTGGATGGGATGGGAAAGGAAACAC 714  
Qy IleAspThrLysTyrValValHis----- 161  
Db 715 TTGAGACAAACTTCACCTTAAATCTGAATGGGCAACACACAGTTTGTCTGATTGCAAA 774  
Qy ValLysSerLeuGluThrGluGluGluGlnIleThrLeuThrSerSerTyrIleAsn 180  
Db 775 GCAAAACGTGACACCCCACTTCAGCTGCTGATTAATTCCTGCTGATTTTGTAC 834  
Qy IleSerThrAspSerLeuGlnGlyLysLysTyrLeuValTyrValGlnAlaIleAsn 200  
Db 835 ATTGAA-----GTCTGGTAGAAGCAGACAAAT 861  
Qy AlaLeuGlyMetGluGluSerLysGlnLeuGlnIleHisIleuAspAspIleVal----- 218  
Db 862 GCCCTTGGAAGGTTACATCAGAT-----CATATCAATTTTGAATCCGTATATATTAAGTG 915  
Qy 219 -----IleProSerAlaIleValIleSerArgIleGluThrIleAsnAlaVal 235  
Db 916 AAGCCCAATCGCCACATTAATTTATCAGTATCACTCAGAGCACTGTCTAGATCTTA 975  
Qy 236 ProLysThrIleIleTyrTyrAspSerGlnThr-----ThrIleGluLysValSerCys 253  
Db 976 AATATGACA-----TGACCAACCAAGATTAAGAGTGTATTAATCTAAATAT 1026  
Qy 254 GluMetArgTyrLysAlaThrThrAsnGlnThrTyrAsn---ValLysGluPheAspThr 272  
Db 1027 AACATTCATATATGACCAAAAGATGCTCACTTGAGGCCAGATTCCTCTCGAAGACACA 1086  
Qy 273 AsnPheThrTyrValGlnGlnSerGluPheTyrLeuGluProAsnIleLysTyrValPhe 292  
Db 1087 GCATCCACCGGATCTTCATTCACGTGCCAGACCACTTAAACCTTTTACAGAAATAGTGTT 1146  
Qy 293 GlnValArgCys---GlnGluThrGlyLysArgTyrTyrGlnProTyrSerSer----- 309  
Db 1147 AGGATTCGCTGTATAGAGAAAGATGTAAGGATACCTGAGTGACTGAGTGAAGAAACA 1206  
Qy 310 -----ProPhePheHisLysThrPro 316  
Db 1207 AGTGGATGACCTATGAAATAGACATCTAAAGCACCACCAAGTTCTGTATTAATAATAGAT 1266  
Qy 317 -----GluThrValPro----- 320  
Db 1267 CCATCCCATCTCAAGGCTACAGACTGTACACTCGTGTGAAAGACATTCCTCTCTTTT 1326  
Qy 321 GlnValThrSerLysAlaPheGlnHisAspThr-----TyrAsnSerGlyLeu 336  
Db 1327 GAAGCCCAATGGAATAATCTTGATTAAGATGACTGTCAACAATGGAATTCACATTTA 1386  
Qy 337 -----ThrVal---AlaSerIleSerThrGlyHisLeuThrSerAsnArgGly 352

Db 1387 CAATAATTACACAGTTAATGCCACAAAACCTGACAGTAATCTCAAAATGATGCC----- 1440  
Qy AspIleGlyLeuLeuLeuGlyMetIleValPheAlaValMetLeuSerIleLeuSerLeu 372  
Db 1441 -----TATCTAGCAACCTTAACAGTAAGAAATCTT 1470  
Qy 373 IleGlyIlePheAsn----- 377  
Db 1471 GTTGGCAATACAGATCAGCTGTTTAACTATCTCCTGCTGTGACTTCAAGCTACTCAC 1530  
Qy 378 -----ArgSerPhe----- 380  
Db 1531 CCTGTAAATGAGATCTTAAGCATTCCTCCCAAGATTAACATGCTTTGGTGAATGAGACTACT 1590  
Qy 381 ---ArgThrGlyIleLysArgArgIleLeuLeuLeuIleProLysTyrLeuTyrGluAsp 399  
Db 1591 CCAAGGAATCTGTAAAGAAATATATATCTT-----GAGTGGTGT----- 1629  
Qy 400 IleProAsnMetLysAsnSerAsnValValLysMetLeuGlnGluAsnSerGluLeu--- 418  
Db 1630 GTGTATCAGATTAAGACACCTGTATCACAGACTGGCAACAGAGATGTACCTGTCAT 1689  
Qy 419 -----MetAsnAsnSerSerSerGluGlnValLeuTyr-----ValAspPro 432  
Db 1690 CGCACTTATTTAAGAGGAACTTAGCAGAGAGAAATGCTTGTATTAACAGTTACTCCA 1749  
Qy 433 MetIleThrGlu-----IleLysGluIlePhe 441  
Db 1750 GTATATGCTGATGAGACCAAGAACCTCGAATCCATAAAGCATACCTTAACAGACT--- 1806  
Qy 442 IleProGluHisLysProThrAspTyrLysLys-----GluAsnThrGlyProLeu 458  
Db 1807 CCACCTTCCAAAGACACTACTGTTCGACAAAAAAGTAGGAAAAACGAAAGCTGTCTTA 1866  
Qy 459 GluThrArgAspTyrPro-----GlnAsnSerLeuPheAsnThrThrVal 475  
Db 1867 GAGTGGACCAACTCTCTGTGATGTTCAGAAATGATTAATTCAGAAATTAATTAATTT 1926  
Qy 476 Tyr----- 476  
Db 1927 TATTAAGAACATCATTTGGAATGAACCTGCTGATATGTGATTCTTCCACAGAAATAT 1986  
Qy 476 ----- 476  
Db 1987 ACATTCCTCTTTGACTAGTGAACATGTGATGATGCAATGGCAGCATACAGAT 2046  
Qy 476 ----- 476  
Db 2047 GAAGTGGGAAGATGTCAGAAATTCATTTACTACCCCAAGTTTGCTCAAGAGAA 2106  
Qy 476 ----- 476  
Db 2107 ATTGAAGCATAGTCGTGCTGTGTTGCTTAGCATTCCTATTGACAACTCTTGGAGATG 2166  
Qy 477 -----IleProAsp 479  
Db 2167 CTGTTCTGTTTATTAAGACAGACTTAATTAACAAACATCTGCTTAATGTTCAGAT 2226  
Qy 480 LeuAsnThrGlyLysProGlnIleSer-----AsnPheLeu 492  
Db 2227 CTTCAAAAGATCATATTCCTCAGGTGTACCTTCACACTCTCCCAAGACCAATTTAAT 2286  
Qy 493 ProGluLysSerHisLeuSerAsnAsnAsn-----GluIleThr 505  
Db 2287 TCAAAAGATCAAAATGATTAATGATGCGCAATTTCACTGATGCTAAGTGTGGAATAGAA 2346  
Qy 506 SerLeuThrLeuLysPro---ProValAsp-----SerLeuAsp----- 517  
Db 2347 GCAAAATGACAAAAGCCTTTTCCAGAAAGATGTGAATCATTTGACCTGTTCAAAAGAAA 2406  
Qy 518 -----SerGlyAsnAsnProAsnGluLys 526  
Db 2407 AAAATTATATCTGAAGACACACAGACTGTATTGGGGGGGCTTCATGATGATCTTCT 2466



Db 259 TTGAGCTTGCAACCTTGGTAGTGCAGAGCTTGTTATTCTTCTCASCAGTAACTTACA 318

Qy 24 GilylIethrAsnIleasnCyserGlyHisIleTrrValGluProAlaThrIlePheIys 43

Db 319 GGTGAACCTTGTAGATCCAGT---GGTATATACAGTCTGAA---TCTCAGTGTGACA 372

Qy 44 MetGlyMetAsnIleSerIleTyrCyserGlnIalaIleIysAsnCyserGlnProArgIys 63

Db 373 CTTCATCTGTAATTTCACTGCAGTTGT-----GTCCTAAAGAAAAATGTATGATTTAT 426

Qy 64 LeuHlsPheTyrIysAsnGlyIle-----LysGlu 73

Db 427 TTTGATGTAATAAGTAAATTACATTTGTCTGGAAACAAACCATTTTACTATTCTTAAGGAG 486

Qy 74 ArgPheGlnIleThrArgIleAsnIlyThrIlaIAsnIleTrrIyIysAsnPheIeu 93

Db 487 CAATGTACTATC---ATMAACAGAACAGCATAGTGCACCTTTCACAGTAAATAGCT 540

Qy 94 GluProHlsAlaSerMetTyrCyserThrIaGluCyserProIyHlsPheGlnIuTrrIeu 113

Db 541 TCATTAATATTCACTCACTCACTTCAACTCTTACATTCGGACAGCTTGAACGAT--- 597

Qy 114 IleCyserGlyIysAspIleSerSerGlyTyrProProAspIleProAspGluValThrCy 133

Db 598 GTTATGGAATACATATATTTCAGGCTTGCTCCAGAAAACCTTAAATTTGAGTTGC 657

Qy 134 ValIleTyrGluTyrSerGlyAsnMetThrCyserThrTrrAsnAla\*\*LysIleuTrrTyr 153

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Qy 154 IleAspTrrIyTyrValValHls----- 161

Db 715 TTGGAGACAAACTTCACTTAAATCTGAATGGCAACACAGATTTCTGATTCGAA 774

Qy 162 ---ValIysSerLeuGlnThrGluGluGluGlnIyTrrIeuThrSerSerTrrIleAsn 180

Db 775 GCMAAACGTGACACCCCACTCATGCACTGTGATTAATTCACTGTGATTTGTTCAC 834

Qy 181 IleSerThrAspSerLeuGlnGlyGlyIyIysIyTrrIeuValTrrValGlnIlaIlaAsn 200

Db 835 ATTTGAA-----GTCGTGGTAAAGCAGAGAAAT 861

Qy 201 AlaIleuGlyMetGluGluSerIyGlnIeuGlnIleHlsIleAspAspIleVal----- 218

Db 862 GCCCTTGGGAAGTTACATCAGAT-----CATATCAATTTTGACCTCTATATAAAGT 915

Qy 219 -----IleProSerAlaIlaValIleSerArgIaGluTrrIleAsnAlaThrVal 235

Db 916 AAGCCCAATCCGCGCATATTTATCAATGATCACTACAGAGAACTGTCTGATCTTA 975

Qy 236 ProIySerThrIleIleTyrTrrAspSerGlnThr-----ThrIleGluIyValSerCy 253

Db 976 AAATTGACA-----TGGACCAACCAAGTATTAAGAGGTATTAATTACTAAATAT 102

Qy 254 GluMetArgTyrIysAlaThrThrAsnGlnThrTrrAsn---ValIysGluPheAspThr 272

Db 1027 AACATTCATATAGACCAAGATGCCCACTTGAGCAGATTCCTCTGAAGACACA 108

Qy 273 AsnPheThrTyrValGlnGlnSerGluPheTyrIleuGluProAsnIleIyIysTrrValPhe 292

Db 1087 GCATCCACCCGATCTTCATCACTGTCGCAAGCATTAACCTTTTACAGAAATATGTGT 1144

Qy 293 GlnValAsyCyS---GlnGluThrGlyIysAspGlyTrrIleGlnProTrrSerSerProPhe 311

Db 1147 AGGATTCCTGTATAGAGAAAGATGTATAGGATCTCGAGTGCATCGAGTAAGAAGACA 1200

Qy 312 PheHlsIyThrProGlu---ThrValPro-----GlnValThrSerIyysAlaPheG 328

Db 1207 AGTGGATCATCCTATAGATTAACATTCCTCTTTTGAAGCCAAATGAAAATCTTGA 126

Qy 328 nHlsAspThr-----TrrAspSerGlyIeu-----ThrVal---AlaSe 340

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Db      1267 TTATGAGTCACTCTCAAGATGAAATACATTTCACAAATTATACACAGTTAATGCCAC 1326
Qy      340 rIleSerThrGlyHisLeuThrSerAspAsnArgGlyAspIleGlyLeuLeuLeuGlyMe 360
Db      1327 AAAACGACAGTAATCTCAACAAATGATCCG----- 1357
Qy      360 tIleValPheAlaValMetLeuSerIleLeuSerIleGlyIlePheAsn----- 377
Db      1358 -----TATCTAGCAACCCCTAACAGTAAGAAATCTTTGGCAATACAGATGCAGCTGT 1410
Qy      378 ----- 380
Db      1411 TTTAATATCCCTGCTGTGATCTTTCAAGCTATCACTCCGTGAATGATCTTTAAAGCAT 1470
Qy      380 e-----ArgThrGlyIleLysArg 387
Db      1471 CCCCAAGATTAACATGCTTTGGGTGGAATGATGATCTCAAGGAATCTGTGAAGAAATA 1530
Qy      387 gIleLeuLeuLeuIleProLysTrpLeuTrpGluAspIleProAsnMetLysAsnSerAs 407
Db      1531 TATACTT-----GAGTGGTGT-----GTGTTATCAGATTAAGCACCCCTG 1569
Qy      407 nValValLysMetLeuGlnGluAsnSerGluLeu-----MetAsnAsnAsn 423
Db      1570 TATCAGACAGCTGCGACAGAAAGATGGTACCGTGATCGACCTATTTAAGAGGAACTT 1629
Qy      423 rSerGluGlnValLeuTrp-----ValAspProMetIleThrGlu----- 436
Db      1630 AGCAGAGAGCAATGCTATTGATATACAGTTACTCCAGTATATCTGATGACCAAGAG 1689
Qy      437 -----IleLysGluIlePheIleProGluIleLysProThrAs 449
Db      1690 CCCTGAATCCATAAGCATACCTTTAAACAAGCT-----CCACCTTCCAAGAGACCTACTGT 1746
Qy      449 pTyrLysLys-----GluAsnThrGlyProLeuGlnThrArgAspTrpPro----- 464
Db      1747 TCGACACAAAAGTAGGAGAAAAGCAAGCTGCTCTTGAAGGAGCAACTTCTGTGGA 1806
Qy      465 -----GlnAsnSerLeuPheAspAsnThrValValValTrp----- 476
Db      1807 TGTTCAGATGATTTATCAGAAATTATATATTTTATTAAGAACCATATTGAAATGA 1866
Qy      476 ----- 476
Db      1867 AACTGCTGTGATGTGATTTCTCCACACAGAAATATATATGCTCTTGACTAGTA 1926
Qy      476 ----- 476
Db      1927 CACATTTGACATGGTACGAATGGACATACACAGATGAGTGGAGAGATGCTCCAGA 1986
Qy      476 ----- 476
Db      1987 ATTCACTTTACTACCCAAAGTTTGTCAAGAGAAATTGAAGCATAGTCGTGCTGT 2046
Qy      476 ----- 476
Db      2047 TTGCTTAGCATTCCTATTTGACAACTCTTCTGGAGTGTCTGTCTTAAATAAGCAGA 2106
Qy      477 -----IleProAspLeuAsnThrGlyTrpLysProG 487
Db      2107 CCTAATTAATAAACACATCTGGCCTAATGTTCCAGATCTCTTCAAGAGTCATATTTGCCCA 2166
Qy      487 nIleSer-----AsnPheLeuProGluGlySerHisLeuSerAs 500
Db      2167 GTGTACACTCACTCACTCTCCAGGACAAATTTTAATTCAAAGATCAAATGTAATCCAGA 2226
Qy      500 nAsnAsn-----GluIleThrSerLeuThrLeuLysPro--Pr 512
Db      2227 TGGCAATTTCACTGATGTAAGTGTGTGGAAATAGAGCAATGACAAAAGCCTTTTCC 2286
Qy      512 oValAsp-----SerLeuAsp----- 517
Db      2287 AGAAGATCTGAATCAATTCATTTGACCTGTTCAAAAAGAAAAATTAATACTGAAGACACAG 2346

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Qy      518 -----SerGlyAsnAsnProArgLeuGlnLysHisProAsnPheAlaPheSerVal 534
Db      2347 CAGTGGATATGGGGGGGCTTTCATGATGATGATCTTCTAGGCGCAAGCATTTCTAGCAGTGA 2406
Qy      534 lSerSerValAsnSerLeuSerLeuSerLeuThrIlePheLeuGlnGlyLeuSerLeuLeuAs 554
Db      2407 TGAAGATGAATCTTCA-----CAAAACACTTCGACACCTGCTCCAGATTTCTACCGGTGACA 2463
Qy      554 ngInGly---GluCysSerSerProAspIleGln---AsnSerValGluGlnLysThrTh 572
Db      2464 CAGTGGCTACAGACACCAAGTTCTCTCAGTCAGTCAGTCTTCAAGATCCAGATCTACCCA 2523
Qy      572 rMetLeuLeuGluAsnAspSerProSerGlnThrIleProGluGlnThrLeuLeuProAs 592
Db      2524 GCCCTGTATTAGAT-----TCAGAGAGCGCGCGAAGAGATCTACAAATTAGTAGA 2571
Qy      592 pGluPheValSerCysLeuGlnGlyIleValAsnGlnGlnLeuProSerIleAsnThrTrp 612
Db      2572 TCATGTAGATGGCGGTGATGTATTTTGGCCAGGCA-----CAGTACTT 2616
Qy      612 eProGlnAsnIleLeuGlu-----SerHisPheAsnArg 623
Db      2617 CAACACAGACTGCGACGTCAGCATGATCCAGATTTTCACTTTGAAAG 2671

RESULT 10
US-11-330-726-179
: Sequence 179, Application US/11330726
: Publication No. US20060204982A1
: GENERAL INFORMATION:
: APPLICANT: Engelhard, Eric
: APPLICANT: Morris, David
: TITLE OR INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
: FILE REFERENCE: 20366-011002
: CURRENT APPLICATION NUMBER: US/11/330,726
: PRIOR FILING DATE: 2006-01-12,482
: PRIOR APPLICATION NUMBER: US 10/052,482
: PRIOR FILING DATE: 2001-11-08
: PRIOR APPLICATION NUMBER: US 09/747,377
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: US 09/798,586
: PRIOR FILING DATE: 2001-03-02
: NUMBER OF SEQ ID NOS: 241
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 179
: LENGTH: 2723
: TYPE: DNA
: ORGANISM: Homo sapiens
US-11-330-726-179

Alignment Scores:
Pred. No.: 2,93e-08 Length: 2723
Score: 190.00 Matches: 144
Percent Similarity: 34.7% Conservative: 82
Best Local Similarity: 22.1% Mismatches: 228
Query Match: 5.7% Indels: 197
DB: Gaps: 35

US-10-667-289-2 (1-629) x US-11-330-726-179 (1-2723)
Qy      104 GluCySerProLysHisPheGlnGlnThrLeuIleCysGlyLysAspIleSerSerGlyTrp 123
Db      272 GAAGGACGACCAATGAGAAATGATGCGATCGCAACCGTTTCACTCTGCTACTTTT 331
Qy      124 ProProAspIleProAspGluValThrCysValIleTrpLys----- 137
Db      332 TTCACACCTGCGCTCTCTGATGACAGCTTACCTCTCGGAAACCTGAGATCTTTAATG 391
Qy      138 ---TyrSer-----GlyAsnMet-ThrCysThrTrpAsnAla**LysLeuThrTrp 154
Db      392 TCGTCTCCCAATAGGAACCAATTCACCTCTGTGTGAGGCGTGGGACAAATGAGAGACT 451
Qy      154 eAspThrLysTrpValValHisValLysSerLeuGlnThrGlnGlnGlnLysLys 174

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; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 109
; LENGTH: 2736
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-669-920-109

Alignment Scores:
Pred. No.: 2,95e-08 Length: 2736
Score: 190.00 Matches: 144
Percent Similarity: 34.7% Conservative: 82
Best Local Similarity: 22.1% Mismatches: 228
Query Match: 5.7% Indels: 197
Gaps: 35
DB:

US-10-667-289-2 (1-629) x US-10-669-920-109 (1-2736)

QY 104 GluCyseProlyshisPheGlnGluThrLeuIleCysGlyLysAspIleSerSerGlyTyr 123
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 285 GAAGGACAGCCAAACATGAAGAAATGTGGCATCTGCAACCGTTTCACTGCTACTTTT 344

QY 124 ProProaspIleProAspGluValThrCysValIleTyrGlu----- 137
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 345 TCTCAACACCTGCTCTGAAATGAGACAGTTACTCTCGAAAACCTGAGATCTTTAAATG 404

QY 138 ---TyrSer-----GlyAsnMet-ThrCysThrTyrAsnAla**LysLeuThrTyrI 154
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 405 TCGTCTCCCAATAAGAAACATTCACCTGCTGTGTGAGAGCCCTGGACAGATGGAGACT 464

QY 154 eAspThrLysTyrValValHisValLysSerLeuGlnGluGlnGlnTyrLe 174
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 465 TCCTACCAATATAT-----TCACGACTTACCAAGGAGGAGAGAGACACT 509

QY 174 u-----ThrsSerTyrIleAsnIleSer-ThrsAspSerLeuGlnGlyLys 191
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 510 CATGCATGATATGCCAGACTACATACCGGTGGCCCACTCTGCCACTTTGGCAAGCA 569

QY 191 s-----TyrLeuValTyrValGlnAlaAlaAsnAlaLeuGlyMe 204
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 570 GTACACCTCCATGTCGAGACATACATCATGATGTCAATGCCACTAACGATGGAG 629

QY 204 tGluGlnSerLysGlnLeuGlnIleHisLeuAspAspIleValIleProser----- 221
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 630 CAGTTCTCCGATAACTTATATGTGACGTGACTTACATGTCAGCCAGACCTCTCTT 689

QY 222 -----AlaAlaValIleSerArgAlaGluThrIleAsnIleThrValProlysthrI 239
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 690 GGAAGCTGGCTGTGAAGTAAACAGCCAGAAC-----AGAAAACCTTACTGTG 740

QY 239 eIleTyrTyrAspSerGlnThrThrIleGlu-----LysValSerCy 253
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 741 GATTAAATGTGTCCACCTACCTGATTTGACTTTAAAACTGTGTGTTACCGCTCCGTGA 800

QY 253 eGlnMetArgTyrLysAlaThrThrAsnGlnThrTyrAsnValLysGluPheAspThrAs 273
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 801 TGAATATTCGATTAACCCGAGAAAGCAGTGAAGTGGAGATC-----CA 845

QY 273 nPheThrTyrValGlnGlnSerGluPhe-----TyrLeuGluProAsnIleTyr 290
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 846 TTTTGTCT--GGGACGACAAACAGAGTTTAAGATTCTCAGCTTACATCCAGAGCAAGATA 902

QY 290 rValPheGlnValLysCysGlnGlnThrGlyLysArgTyrTyrGlnProTyrSerSerPr 310
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 903 CCTGTGTCAAGTTTGGCTGC---AAACGACACATGATATCTGAGTGTGATGAT----- 954

QY 310 oPhePheHisLysThrProGluThrValProGlnValThrSerLysAlaPheGlnHisAs 330
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 955 -----CCAGCGACCTTCATTCAGATACCTAGTACCTTCAACATGAAATGA 998

QY 330 pThr-----TyrAsnSerGlyLeuThrValAlaSerIleSerThrGlyHisLeuThrse 348
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 999 TACAACCGTGTG-----ATCTGTGTGCTGTCTTCT----- 1032

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QY 348 rAspAsnArgGlyAspIleGlyLeuLeuGlnGlyMetIleValPheAlaValMetLeuSe 368
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1033 -----CGTGCATCTGTGTGATATATGTCTGGGACGAGCTTTGAA 1073

QY 368 rIleLeuSerLeuIle-----GlyI 375
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1074 GGGCTATATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1133

QY 375 ePheAsnArgSerPheArgThrGlyIleLysArgArgIleLeuLeuLeuIle----- 392
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1134 TGATGCTCATCTGTGTGAGAAAGGCAAGTGTGAAGAACTACTAGTCCCTTGGAGTCCA 1193

QY 393 -----ProLysTyrLeuTyrGluAspIleProAsnMetLysAsnSerAsnValVa 409
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1194 AGACTTCTCTCCCACTTCTGACTATGAGACTTG-----CTGGT 1232

QY 409 lLysMetLeuGln-----GluAsnSerGluLeuMetAsnAsnSerSerG 425
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1233 GAGATATTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1292

QY 425 u-----GlnValLeuTyrValAspPro----- 432
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1293 ACACCCAAAGTCAAGTATGAAACCCACATACCTGATCTGACACTGACTAGCCGAGG 1352

QY 433 -----MetIleThrGluIleLysGluIlePheIleProGluHisLys 446
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1353 GAGCTGTGACAGCCCTCTCTTGTGTGTAAGATGTGAG-----GAAACCCAGGCCAA 1406

QY 446 sProThrAspTyr-----LysLysGluAsnThrLysProLeuG 459
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Db 1407 TCCCTCCACATTTGATGATCTTGAAGTATGATGAAAGCCAGAAATCTGAAACCA 1466

QY 459 uThrArgAspTyrProGlnAsnSerLeuPheAspAsnThrThrValValTyrIleProAs 479
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1467 CACTGTGAGC-----CCCAAGTGCATTAACATGAAAGCCAA-----ATCCCTTA 1511

QY 479 pLeuAsnThrGlyTyrLys-----ProGlnIleSerAsnPheLe 492
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Db 1512 TTTTCATGCTGTGTGATATCCAAATGTTCAACATGAGCCCTTACCAAGCCGACAGCAA 1571

QY 492 uProGluGlySerHisLeuSerAsnAsnGlnIleThrSerLeuThrLeuLysPro-- 511
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1572 CCCCAATCTCTTAC--CACAAATATTACTATGTGTGTGAGCTGTGTGTGAGCTGTGC 1628

QY 512 -----ProValAspSerLeuAspSerGlyAsnAsnProArgLeuGlnLysHisProAs 529
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1629 AGGTGCACCGGCACCTCTGTGATGATGAAGCAAGTAAAGATCTTAAATCC----- 1680

QY 529 nPheAlaPheSerValSerSerValAsnSerLeuSerAsnThrIlePheLeuGlnGluLe 549
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Db 1681 -----TTCAAACCATTAAGCTAGAGAGA 1706

QY 549 uSerLeuIleLeuAsnGlnGlyLysCysSerSerProAspIleGlnAsnSerValGlnG 569
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QY 589 uLeuProAspGluPheVal-----SerCysLeuGlyIleVa 601
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Db 1809 TAAACCTTGATATATGTGAGATTCACAAGTCAACAAGATGTGTCAATATCATATGCT 1868

QY 601 l-----AsnG 603
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QY 603 uGluLeuProSerIleAsnThrTyrPheProGlnAsnIleLeu-----Glyse 619
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Db      966 CCAGCATCTAATGTCAGTCATTCATAAAGAACACCAAGTATGAAACCACTA 1025
Qy      429 rValAspPro-----MetIleThrG1 436
Db      1026 CTTGGATCTCGACACTGACTGAGCCGGGAGCTGTGACAGCCCTTCCCTTTGGTCTGA 1085
Qy      436 uilelygluilephehellleprogluH1slyeProThrAspIyr----- 450
Db      1086 AAATGTGAG-----GACCCTCAGGCCAAATCCTCCACATTCATATGATCTGAGTCAT 1139
Qy      451 ----LyslyeGluAsnThrGlyProLeuGluThrArgAspIyrProGluAsnSerLeuPh 469
Db      1140 TGAGAACCCAGAGATCTGTAACCAACCCACCTGGAGC-----CCCGAGTCATATAGCAT 1196
Qy      469 eAspAsnThrThrValValIyrIleProAspLeuAsnThrGlyIyrIys----- 485
Db      1197 GGAAAGGCAA-----ATCCCTATTTTCATGCTGTGATCCAAATGTTCAAC 1244
Qy      486 -----ProGluIleSerAsnPhelLeuProGluIlySerH1sLeuSerAsnAsnAs 502
Db      1245 ATGGCCCTTACCAACGCCACGACACACCCAGATCCTTAC---CACATATATAC 1301
Qy      502 ngulilethserleuthrleuIyPro-----ProValAspSerLeuAspSerG1 519
Db      1302 TGATGTGTGTGAGCTGGCTGTGGCCCTGACAGTGCACCGGCACTGTGTAATGAAGC 1361
Qy      519 yAsnAsnProArgLeuGluIlysh1sProAsnPhelAspSerValSerSerValAsnSe 539
Db      1362 AGGTAAAGATGCTTAAATCC----- 1383
Qy      539 rLeuSerAsnThrIlePheLeuGlyGluLeuSerLeuIleLeuAsnGlnGlyIyCyse 559
Db      1384 ----TTCAAACCACTTAAGTTAGAGAAAGAGGAAAGCAACCAAGAGAGGAGTGA 1439
Qy      559 rSerProAspIleGlnAsnSerValGluGluGluThrThrMetLeuGluAsnAspSe 579
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Qy      579 rProSerGluThrIleProGluGlnThrLeuLeuProAspGluPheVal----- 595
Db      1483 -CCCCAGAGAGAAAACCCCTTGGCTCGCTAAACCTTGGATATATGAGATTCAAA 1541
Qy      596 -----SerCyseLeuGlyIleVal----- 601
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Qy      602 -----AsnGluGluLeuProSerIleAsnThrIyrPhePr 613
Db      1602 CAAGAAGCCGGGACTCCTGAGAACATTAAGAGTATGCAAGGTGTCCGGGTCATGGA 1661
Qy      613 oglnAsnIleLeu-----GluSerH1sPheAsnArgIleSerLeuLeuGly 629
Db      1662 TAAACAACATCTGTGTGTGTGTGTCAGATTCACATGCTAATAAAACGTGGCTTGTGAAGA 1721
Qy      629 s 629
Db      1722 A 1722

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; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3101
; LENGTH: 5252
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-3101

Alignment Scores:
Pred. No.: 1,18e-07 Length: 5252
Score: 188.00 Matches: 109
Percent Similarity: 36.0% Conservative: 68
Best Local Similarity: 22.2% Mismatches: 184
Query Match: 5.7% Indels: 130
DB: Gaps: 26

US-10-667-289-2 (1-629) x US-10-511-937-3101 (1-5252)
Qy      111 GluThrLeuIleCyseGlyLyAspIleSerSerGlyIyrProProAspIleProAspGlu 130
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Qy      131 ValThrCyseValIleIyrGluIyrSerGlyAsnMetThrCysThrTPAsnAla**Lys 150
Db      1168 CTGAATTGTAGACACATGATTTAA--GAATTTATATAGTATGAGATCCAGAAAGG 1224
Qy      151 LeuThrIyrIle-----AspThrLyserIyrVal----- 159
Db      1225 GTGACAGCGTTGGTGGGCCCAAGCTGACAAAGCTTACCTTATGTTGAAGTTTTCAGGA 1284
Qy      160 ----ValH1sValIySerLeuGluThrGluGluGlnGlyIyrLeuThrSerSer 177
Db      1285 AATATGTGTAGACTTAAAGAGCTGAAGCACTTAACAAAGCAAGCTAT----- 1332
Qy      178 TyrIleAsnIleSerThrAspSerLeuGlnGlyIyLyserIyrLeuValTPValGln 197
Db      1333 -----CAATATATTATTCAAATGCTTCCAAATCAAGAAATATATATTATTTACTTGAAAT 1386
Qy      198 AlaAlaAsnAlaLeuGlyMetGluGluSerLyseGlnLeuGlnIleH1sLeuAspAspIle 217
Db      1387 GCTCACAATCCGCTGGTGCATCATCAATCAAAATTTTA---GTTATATATACGAAAAA 1443
Qy      218 ValIleProSerAlaAlaValIleSerArgAlaGluThrIleAsnAlaThrValProLyse 237
Db      1444 GTTATATCCCATACTCTCTACTTCAATCAAGTAGAAGATTTTATTCACACGCTTTAAA 1503
Qy      238 ThrIleIleIyrThrAspSerGlnThrThrIleGluIyValSer-----CysGluMet 255
Db      1504 -----CTTCTTGGCACTTACAGAGCACTTTCAGAAAGATTAATTTTATGTGAAT 1557
Qy      256 ArgTyrlsValaThrThrAsnGlnThrTPAsnValIyGluPheAspThrAsnPheThr 275
Db      1558 GAATTAAGAAATCT-----AATTCACTACAGAGACCGGAAATGTACCA 1602
Qy      276 Tyr-----ValGlnGlnSerGluPheIyr-----LeuGluProAsnIle 288
Db      1603 ATCAAAGAGTGAAGAAATTCAGATTATCTGTGCTGTGCAACAAGTTAATCCATACACT 1662
Qy      289 LyserIyrValPheGlnValArgCyseGlnGluThrGlyIyAspArgIyrTPGlnProTPSer 308
Db      1663 CTATATACCTTTGGATCGTGTGTTCTACTGAAAACCTTTCGAAATGAGCAAAATGAGC 1722
Qy      309 SerProPheH1sLyserIyrProGluThrValProGlnValThrSerIyValaPheGln 328

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Db 1768 CCGATCTCTGGAGA-----GAGTGAAGTTCT 1794
Qy 349 AspAsnArgGlyAspIleGlyLeuLeuGlyMetIleValPheAlaValMetLeuSer 368
Db 1795 GATCGAATA-----AATTATATATCTATGGAAGCCCTTTACCC 1833
Qy 369 IleLeuSerIleuIleGly-----IlePheAsnArgSerPheArgThrGlyIleLeu 385
Db 1834 ATTATATAGAGCTATATGAAAAAATACCTTCCATCATATATCTGCTCATCATAGAGGAA 1893
Qy 386 ArgArgIleLeuLeuLeuIleProlyeTrpLeuTrpGlu---AspIleProAsnMetLeu 404
Db 1894 ACACAGTCCTTTCTGAAATCCCGATCCACAGACAAAGAGAGATACGACTTGATTAAG 1953
Qy 405 AsnSerAsnValValIleValMetLeuGlnGluAsnSer----- 416
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Qy 417 -----GluLeuMetAsnAsnAsn---SerSerGluGlnValLeu----- 428
Db 2014 ATAGCGAGTATGGAATTCACAAATGATGATCTCAAAATAGAACAGTTGTTGGAGTGG 2073
Qy 429 -----TyrValAspProMetIleThrGluIleGlyLeuPhe 441
Db 2074 AAGGGATTCCTCTCACCTGCGATTAAGACCCCAACATGACT----- 2115
Qy 442 IleProGluHisIleValProThrAspTyr-----LysIleGluAsnThrGly 456
Db 2116 -----TGGAGCTACGCTCATTAAGTGGTGTAACTGCTCGGTCGAA 2157
Qy 457 Pro-----LeuGluThrArgAspTyrProGlnAsnSerIlePheAsnThrVal 474
Db 2158 CCAATGCTTATGAGCTGAGAGAAAAGTTCCCTCAACAGCC-----ACTGAATCTGTA 2208
Qy 475 ValIleProAspLeuAsnThrGlyTyrIleProGlnIleSerAsnPheLeuProGlu 494
Db 2209 ATGAATCTGATGAGTTTCGACCGATATAAGA-----TATAATTTTTCCTGTAT 2259
Qy 495 GlySerHisLeuSerAsnAsnGlnIleThrSerLeu-----ThrLeu 509
Db 2260 GGATGCAAAATCAAGATATCAATTTATGCTCCATGATGATATATAGAAATTTG 2319
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Qy 530 PheAlaPheSerValSerSerValAsnSerLeu 540
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/ Sequence 3102, Application US/10511937
/ Publication No. US2006008836A1
/ GENERAL INFORMATION:
/ APPLICANT: EXPRESSION DIAGNOSTICS, INC.
/ APPLICANT: Wohlgenuth, Jay
/ APPLICANT: Fry, Kirk
/ APPLICANT: Woodward, Robert
/ APPLICANT: Ly, Ngoc
/ APPLICANT: Prentice, James
/ APPLICANT: Morris, Macdonald
/ APPLICANT: Rosenberg, Steven
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
/ TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
/ FILE REFERENCE: 506612000104
/ CURRENT APPLICATION NUMBER: US/10/511,937
/ PRIOR FILING DATE: 2004-10-19
/ PRIOR APPLICATION NUMBER: PCT/US2003/012946

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/ PRIOR FILING DATE: 2003-04-24
/ PRIOR APPLICATION NUMBER: US 10/131,831
/ PRIOR FILING DATE: 2002-04-24
/ PRIOR APPLICATION NUMBER: US 10/325,899
/ PRIOR FILING DATE: 2002-12-20
/ NUMBER OF SEQ ID NOS: 3117
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 3102
/ LENGTH: 5252
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (3967)..(3988)
/ OTHER INFORMATION: n t e a, c, g, t o r u
US-10-511-937-3102

Alignment Scores:
Pred. No.: 1.18e-07 Length: 5252
Score: 188.00 Matches: 109
Percent Similarity: 36.0% Conservative: 68
Best Local Similarity: 22.2% Mismatches: 184
Query Match: 5.7% Indels: 130
DB: Gaps: 26

US-10-667-289-2 (1-629) x US-10-511-937-3102 (1-5252)
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Db 1168 GTGAATGTGAGACACATGATTTAA---GAATATATATGTTGAAATCCAGAGAG 1224
Qy 151 LeuThrTyrIle-----AspThrLysTyrVal----- 159
Db 1225 GTGACAGCGTGTGGGCCCACTGCTACAACTACCTTAAGTTGAAAGTTTTCAGGA 1284
Qy 160 -----ValHisValIleValSerLeuGluThrGluGluGlnIleTyrLeuThrSer 177
Db 1285 AAATATGTTAGACTTAAAGAGCTGAAGCCTCAACAAAGAAAGCTAT----- 1332
Qy 178 TyrIleAsnIleSerThrAspSerLeuGlnGlyLysIleValTyrLeuValTrpValGln 197
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Qy 198 AlaAlaAsnAlaLeuGlyMetGluGluSerLysGluLeuGlnIleHisLeuAspAspIle 217
Db 1387 GCTCACATCCGGTGGGTGCATCACATCAACAAATTTTA---GTTAATATACCTGAAAA 1443
Qy 218 ValIleProSerAlaValIleSerArgAlaGluThrIleAsnAlaThrValProLys 237
Db 1444 GTTATCCCATCTACTCTTACTTCAATCAAGTGAAGATTTAATCAACAGCGTTTAA 1503
Qy 238 ThrIleIleTyrTrpAspSerGlnThrIleGluLysValSer-----CysGluMet 255
Db 1504 -----CTTCTTGTCATTTTACAGCAACTTTCGAAAGATTTATTTTATGTGAAT 1557
Qy 256 ArgTyrIleValAlaThrThrAsnGlnThrTrpAsnValIleGluPheAspThrAsnPheThr 275
Db 1558 GAAATTAAGAAACT-----AATTCAAGTACAGAGCAGCGAAATGTGACA 1602
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Qy 289 LysTyrValPheGlnValArgCysGlnGluThrGlyLysArgTyrTrpGlnProTyrSer 308
Db 1663 CTATATATCTTGGATTCCTGTTCTACTGAAACTTTCGAAATGCAACAAATGAGGC 1722
Qy 309 SerProPheHisIleLysThrProGluThrValProGlnValThrSerLysAlaPheGln 328

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Db 1768 CTTGATTAATCTTGAGA-----GAGTGAAGTTCT 1794
QY 349 AspAsnArgGlyAspIleGlyLeuLeuGlyMetIleValPheAlaValMetLeuSer 368
Db 1795 GATGAGAAA-----AATTAAATATCTATTGGAAGCTTTACCC 1833
QY 369 IleLeuSerIleGly-----IlePheAsnArgSerPheArgThrGlyIleLeu 385
Db 1834 ATTATAGAGCTAATGAAAAATCTTCTTCAATGATGATGCTGTCATCAGATGAGGAA 1893
QY 386 ArgArgIleLeuLeuIleProLysTrpLeuTyrglu---AspIleProAsnMetLys 404
Db 1894 ACACAGTCCCTTTCTGAAATCCCTGATCCTCAGACAAAGCAGATACGACTTGATAG 1953
QY 405 AsnSerAsnValValLysMetLeuGlnGluAsnSer----- 416
Db 1954 AATTACTACATCATCAGCTGATGCGTAAATTTCTGGGCTCATCACCACTTCCAA 2013
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Db 2209 ATAGAAATCTGATGAGTTTCGACCAAGGTATAGA-----TATAATTTTCTCTGTAT 2259
QY 495 GlySerHisLeuSerAsnAsnGlnIleThrSerLeu-----ThrLeu 509
Db 2260 GGATGCGAAATCAAGATATCAATTATACGCTCCATGATGATATATGAAGAAATTG 2319
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Job time : 425 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus.p2n model

Run on: October 14, 2006, 14:34:36 ; Search time 312 Seconds

(without alignments)  
5658.305 Million cell updates/sec

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Ygapop 10.0 ,	Ygapext 0.5
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Total number of hits satisfying chosen parameters: 2807332

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents\_NA.\*

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3: /EMC\_Celerra\_SIDS3/prodata/2/ina/6A COMB.seq.\*  
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9: /EMC\_Celerra\_SIDS3/prodata/2/ina/RE COMB.seq.\*  
10: /EMC\_Celerra\_SIDS3/prodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	3324	99.9	2859 3 US-09-853-1808-1	Sequence 1, Appl1
2	256.5	7.7	2995 3 US-09-700-820C-17	Sequence 17, Appl1
3	216	6.5	4040 2 US-08-685-118-1	Sequence 1, Appl1
4	216	6.5	4040 2 US-08-915-495-1	Sequence 1, Appl1
5	216	6.5	4040 2 US-08-914-520-1	Sequence 1, Appl1
6	216	6.5	4040 3 US-09-949-016-1887	Sequence 1887, Ap
7	216	6.5	4040 5 US-09-543-679A-2896	Sequence 2896, Ap
8	216	6.5	6019 5 US-09-543-679A-2897	Sequence 2897, Ap

9	211	6.3	2754 2 US-08-825-558-5	Sequence 5, Appl1
10	211	6.3	2754 3 US-09-312-611-5	Sequence 5, Appl1
11	209	6.3	3085 3 US-09-023-655-1131	Sequence 1131, Ap
12	209	6.3	3085 3 US-09-949-002-47	Sequence 47, Appl
13	208	6.3	3085 3 US-09-949-002-250	Sequence 250, App
14	207	6.2	1977 2 US-08-825-558-3	Sequence 3, Appl1
15	207	6.2	1977 3 US-09-312-611-3	Sequence 3, Appl1
16	207	6.2	3085 3 US-08-795-473B-4	Sequence 4, Appl1
17	207	6.2	3085 3 US-09-439-856-4	Sequence 4, Appl1
18	207	6.2	3477 3 US-09-313-942-25	Sequence 25, Appl
19	207	6.2	3477 3 US-10-282-162-25	Sequence 25, Appl
20	207	6.2	3507 3 US-09-313-942-23	Sequence 23, Appl
21	207	6.2	3507 3 US-10-282-162-23	Sequence 23, Appl
22	206	6.2	2369 2 US-07-797-556-1	Sequence 1, Appl1
23	206	6.2	2369 2 US-08-108-881-1	Sequence 1, Appl1
24	206	6.2	2369 2 US-09-058-263-1	Sequence 1, Appl1
25	206	6.2	2369 2 US-09-059-099-1	Sequence 1, Appl1
26	206	6.2	2369 3 US-09-058-264-1	Sequence 1, Appl1
27	206	6.2	2369 3 US-09-455-962-1	Sequence 1, Appl1
28	206	6.2	2369 7 PCT-US95-06530-1	Sequence 1, Appl1
29	190	5.7	2724 3 US-09-949-016-4257	Sequence 4257, Ap
30	188	5.7	3182 2 US-07-797-556-5	Sequence 5, Appl1
31	188	5.7	3182 2 US-07-943-843-1	Sequence 1, Appl1
32	188	5.7	3182 2 US-08-347-003-1	Sequence 1, Appl1
33	188	5.7	3591 2 US-07-943-843-5	Sequence 5, Appl1
34	188	5.7	3591 2 US-08-347-003-5	Sequence 5, Appl1
35	188	5.7	5245 3 US-09-949-016-4210	Sequence 4210, Ap
36	188	5.7	5252 3 US-09-949-016-338	Sequence 338, App
37	188	5.7	5252 3 US-10-131-827-8827	Sequence 8827, Ap
38	188	5.7	5252 3 US-10-131-827-8828	Sequence 8828, Ap
39	188	5.7	5252 5 US-10-131-831-8827	Sequence 8827, Ap
40	188	5.7	5252 5 US-10-131-831-8828	Sequence 8828, Ap
41	181.5	5.5	3293 2 US-07-923-976-1	Sequence 1, Appl1
42	171.5	5.2	2498 2 US-07-943-843-3	Sequence 3, Appl1
43	171.5	5.2	2498 2 US-08-347-003-3	Sequence 3, Appl1
44	170.5	5.1	1724 3 US-09-071-224-5	Sequence 5, Appl1
45	168.5	5.1	1218 3 US-09-012-072-1	Sequence 1, Appl1

#### ALIGNMENTS

RESULT 1  
US-09-853-1808-1  
? Sequence 1, Application US/09853180B  
? Patent No. 6756481  
? GENERAL INFORMATION:  
? APPLICANT: Chirica, Madeline  
? APPLICANT: Parham, Christi L.  
? APPLICANT: Kastelein, Robert A.  
? APPLICANT: Moore, Kevin W.  
? TITLE OR INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods.  
? FILE REFERENCE: D01074  
? CURRENT APPLICATION NUMBER: US/09/853.180B  
? PRIOR APPLICATION NUMBER: 2001-05-10  
? PRIOR FILING DATE: 2000-05-10  
? NUMBER OF SEQ ID NOS: 4  
? SOFTWARE: PatentIn version 3.2  
? SEQ ID NO 1  
? LENGTH: 2859  
? TYPE: DNA  
? ORGANISM: Homo sapiens  
? FEATURE:  
? NAME/KEY: CDS  
? LOCATION: (119)..(2005)  
? FEATURE:  
? NAME/KEY: misc feature  
? LOCATION: (127)..(127)  
? OTHER INFORMATION: k means g or t/u.  
? OTHER INFORMATION: originally filed.  
? FEATURE:  
? NAME/KEY: mat peptide  
? LOCATION: (188)..(2005)

See page 12, line 34, of patent application at

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FEATURE:
; NAME/KEY: misc feature
; LOCATION: (563)..(563)
; OTHER INFORMATION: x means g or a. See page 12, line 36, of patent application as
; OTHER INFORMATION: originally filed.
US-09-853-180B-1

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Alignment Scores:
Pred. No.: 0 Length: 2859
Score: 3324.00 Matches: 629
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 99.9% Indels: 0
DB: 3 Gaps: 0

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US-10-667-289-2 (1-629) x US-09-853-180B-1 (1-2859)

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QY 1 MetAsn***ValThrIleGlnTPRAspAlaValIleAlaLeuTYrIleLeuPheSerTrp 20
DB 119 ATGATCAAGTCACTATTCAATGGAGATGAGTAATACCCCTTACATACCTTCAAGCTGG 178
QY 21 CysHISGLYGLYIleThrAsnIleAsnCySerGlyHISileTrpValGluProAlaThr 40
DB 179 TGTCATGAGAGAAATTACAAATATAATCTGCTGGCCATCTGGTGAGAACCAAGCCACA 238
QY 41 IlePheIleMetGlyMetAsnIleSerIleTYrCysGlnAlaAlaIleIleAsnCyGln 60
DB 239 ATTTTAAGATGGGTATGAATATCTCTATATATGCCAAGACAGCAATTAAGAATCGCAA 298
QY 61 ProArgIleLeuHISpHeTYrIleAsnGlyIleIleGluArgPheGlnIleThrArgIle 80
DB 299 CCAAGGAACCTCAATTTTATAAATAAGCATCAAGAAGATTTCAATCAACAAGATT 358
QY 81 AsnIleThrThrAlaArgLeuTrpTYrIleAsnPheLeuGluProHISAlaSerMetTYr 100
DB 359 AATTAACAACAGCTCGGCTTGGTATTAATAAATCTTTCGAAACCAATGCTTCTATGTAC 418
QY 101 CysThrIleGluCysProIleAsnIlePheGlnIleuThrLeuIleCysGlyIleAspIleSer 120
DB 419 TGCACTGCTGAATGCCAACAATTTCAAGAGACACATGATATGTGAAAAGACATTCT 478
QY 121 SerGlyTYrProProlaArgIleProAspGluValIleCysValIleIleTYrGluTYrSerGly 140
DB 479 TCTGGAATATCGCCAGATATCTCGATGAAGTAACCTGTGCATTTATGAAATATTCAGGC 538
QY 141 AsnMetThrCysThrTPRAsnAla***IleLeuThrTYrIleAspTrpIleValIle 160
DB 539 AACATGACTTGCACTGGAATGCTRGGAAGCTCACTACATAGACAAATATACGTGTA 598
QY 161 HisValIleSerIleuGluIleuGluGluGluGluGluIleuTYrLeuThrSerSerTYrIleAsn 180
DB 599 CATGTGAAGAGTTTAGAGACAGAGAAGAACAGATATCTCACTCAAGCTATATATTAAC 658
QY 181 IleSerThrAspSerIleuGluGlyIleIleIleIleIleValIleTPRValGlnAlaAsn 200
DB 659 ATCTCCACTGATTATTAACAAGTGGAAGTAAGTGTGGTTCGCAAGCAAGCAAAC 718
QY 201 AlaLeuGlyMetGluIleuSerIleuGluIleuGluIleuIleIleIleAspAspIleValIlePro 220
DB 719 GCATTAAGCATGAGAGAGTCAAAACCACTGCATTAATCTGATGATATAGTATACCT 778
QY 221 SerIleAlaValIleSerArgAlaGluThrIleAsnAlaThrValIleProIleIleIle 240
DB 779 TCTCAACCGCTCATTTCCAGGGCTGAGACTATAATGCTACAGGCCCAAGACCATATAT 838
QY 241 TYrTPRAspSerGlnThrThrIleGluIleValIleSerCysGluMetCysGlyIleAlaThr 260
DB 839 TATTTGGATAGTCAAAACAATGAAAGGTTTCTGTGAAAGAGATACAAAGCTTACA 898
QY 261 ThrAsnGlnThrTPRAsnValIleGluPheAspThrAsnPheThrTYrValGlnGlnSer 280
DB 899 ACNAAACCAACTTGGAATGTTAAAGAAATTTGACCAATTTTACATATGTGCAACAGTCA 958

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QY 281 GluPheTYrLeuGluProAsnIleIleTYrValIlePheGlnValIleCysGluGluIleuThrGly 300
DB 959 GAATTTCTACTGGAGCCAAACATTAAGTACGTATTTTCAAGTGAAGTCAAGAAACAGGC 1018
QY 301 IysArgTYrTrpGlnProTPRAspSerProPhePheHISIleuThrProGluThrValIlePro 320
DB 1019 AAAAGTACTGGAGCCCTTGAGGTTCACCGTTTTCATTAACACCTGAAACAGTTCCC 1078
QY 321 GlnValThrSerIleAsnIlePheGlnHISAspThrTPRAsnSerGlyIleuThrValIleSer 340
DB 1079 CAGTACATCAAAAGACATTCACAAATGACACATGAAATTCCTGGGCTTAACAGTTGCTCC 1138
QY 341 IleSerThrGlyHISIleuThrSerAspAsnArgGlyAspIleGlyIleuLeuGlyMet 360
DB 1139 ATCTTAACAGGACCTTACTTCTGACACAGAGAGACATTTGACCTTTATTTAGGAATG 1198
QY 361 IleValPheAlaValIleMetLeuSerIleIleuSerIleIleGlyIlePheAsnArgSerPhe 380
DB 1199 ATGCTTTCCTGTATGTTGTCAATTTCTTTGATTTGGATATTTAAACATCATTC 1258
QY 381 ArgThrGlyIleIleAsnArgIleIleuLeuIleIleProIleTrpLeuTYrIleAspIle 400
DB 1259 CGAAGCGGATTAAGAAGATCTTATTTGTAATCCAAAGTGGCTTATGAAATATAT 1318
QY 401 ProAsnMetIleAsnSerAsnValIleIleMetLeuGlnIleAsnSerGluLeuMetAsn 420
DB 1319 CCTAATATGAAAAACAGCAATGTTGGAATAATCTACAGAAAAATAGTAACTTAAGAAAT 1378
QY 421 AsnAsnSerSerGluGlnIleValIleuTYrValIleAspProMetIleThrGluIleIleGluIle 440
DB 1379 AATTAATTCAGTACAGAGTCTTATATGTTGATCCCATGATTCACAGATTAAGAAATC 1438
QY 441 PheIleProGluHISIleAsnProThrAspTYrIleIleGluIleAsnThrGlyProLeuGluThr 460
DB 1439 TTCACTCCAAACACAAAGCTTACAGACTACAAAGAGAGATACAGAACCCCTGAGACA 1498
QY 461 ArgAspTYrProGluAsnSerIleuPheAspAsnThrThrValValIleIleProAspLeu 480
DB 1499 AGAGACTACCCGCAAACTCGCTATTTGCAAAATCTACAGTTGTTATATATCTCTGATCTC 1558
QY 481 AsnThrGlyTYrIleAsnProGluIleIleSerAsnPheLeuProGluIleSerHISLeuSerAsn 500
DB 1559 AACCTGGATATTAACCCCAATTTCAATTTTCTGCTGAGGAAAGCCATCTCAAGCAT 1618
QY 501 AsnAsnGluIleThrSerLeuThrIleuIleAsnProProValAspSerIleuAspSerGlyAsn 520
DB 1619 AATTAAGAAATTAATCTCTTAACACTTAACCAACCAAGTTGATCTTAGACTCAGAAAT 1678
QY 521 AsnProArgLeuGlnIleIleAsnPheAlaPheSerValIleSerSerValIleAsnSerLeu 540
DB 1679 AATCCCAAGTTACAAAGACATCTTAATTTGCTTTTCTGTTTCAAGTGTGAATTCATTA 1738
QY 541 SerAsnThrIlePheLeuGluIleuSerIleuIleuAsnGlnIleGlyCysSerSer 560
DB 1739 AGCAACACATATTTCTTGGAGAAATTAAGCTCATATTAATTAAGAGAAATCAAGTTCT 1798
QY 561 ProAspIleGlnAsnSerValIleGluGluIleuThrMetLeuLeuGluAsnAspSerPro 580
DB 1799 CCGACATACAAAACTCAGTAAAGAGAGAAACCAACATGCTTTTGGAAAATGATTCACCC 1858
QY 581 SerGluThrIleProGluGlnIleuThrLeuIleuProAspGluPheValIleSerCysLeuGlyIle 600
DB 1859 AGTGAACATATTCAGAAACAGACCTGCTTCGAGTGAATTTTCTCTGTTTGGGGATC 1918
QY 601 ValAsnGluIleuProSerIleAsnThrTYrPheProGluAsnIleIleuGluSerHIS 620
DB 1919 GTGAATGAGAGTGGCATTTATTAATCTTATTTTCCACAAATATTTTGGAAAGCCAC 1978
QY 621 PheAsnArgIleSerLeuLeuGluIle 629
DB 1979 TTCAATAGATTTCACTCTTGGAAG 2005

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RESULT 2



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US-09-700-820C-17
Sequence 17, Application US/09700820C
Patent No. 6610485
GENERAL INFORMATION:
APPLICANT: Teuchiya, Masayuki
APPLICANT: Saito, Mikiyoshi
APPLICANT: Onito, Toshiniko
TITLE OF INVENTION: NOVEL METHOD FOR GENE CLONING
FILE REFERENCE: 06501-070001
CURRENT APPLICATION NUMBER: US/09/700,820C
CURRENT FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: PCT/JP99/02341
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: JP 10/138652
PRIOR FILING DATE: 1998-05-20
PRIOR APPLICATION NUMBER: JP 10/279876
PRIOR FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 39
SEQ ID NO 17
LENGTH: 2995
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (29) .. (2839)
US-09-700-820C-17

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TOPOLOGY: linear  
 MOLECULE TYPE: CDNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 641..3226  
 US-08-685-118-1

## Alignment Scores:

pred. No.:	6.13e-13	Length:	4040
Score:	216.00	Matches:	75
Percent Similarity:	41.6%	Conservative:	57
Best Local Similarity:	23.7%	Mismatches:	131
Query Match:	6.5%	Indels:	54
DB:	2	Gaps:	13

US-10-667-289-2 (1-629) x US-08-685-118-1 (1-4040)

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Db 731 GGGGATGTACTGTGAAGCTTCCCATGTATTTACTTGATCCACTGCATATTTACA 790
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 52 CyeGlnAlaAlaIlelysaenCyGlnProAlGlyLeuHIsPheTYrlysaenGlyIle 71
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Db 791 TGC-----TCTTGAAAGCCGAGA----- 808
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Oy 72 LygGlnArgPheGlnIleThArgIleAsnlyeThrAlaArgleuTrpYrlyys--- 90
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Db 809 CAAGGCTGCTTCACTATTCACAGCTAACAGTTA-----ATCCTGTACAAAGTTT 859
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Oy 91 -----AsnPhleugluproHIsAla----- 97
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Db 860 GACAGAAGATCAATTTTACACAGGCCACTCCCTCAATTCTGACAGGCTTTCCC 919
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Oy 98 -----SerMetTYrCyethrAlaGluCyProlyshIsPheGlnIuThrLeu 113
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Db 920 CTGGTACAACTGTGTGTCTGCAAACTGGCCGT---ATCATATGTATGAAATTCAA 976
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Oy 114 IIECYGlylysaenIIESErserGlyTYrProProAsnIIEProAsnIIEValIIEThrCys 133
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Oy 134 ValIIETrpIuThrYserGlyAsnMetThrCysThrTrpAsnAla**IysLeuThrTYr 153
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Oy 154 IIEAspThrlyeTYrValIIEHIsValIIE-----LysSerLeuGluThrGluGlu 170
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1097 TTATACACTGATATCTTACAGCTAAGTGACCAAAATTTAACCTGGCAGAAAGCAA 1156
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 171 GlnGlnIuThrleuThrserTYr-----IIEAsnIIESErThrAspSerLeu 186
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1157 TGTAAAGACATTAATGTGACTATTGGACTTGGACTTGAACCTCAACCTCGATCACT 1216
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Oy 187 GlnGlyIlylysaenTYrLeuValIIETrpValIIEAlaAsnAlaIIEugIlyMetGluGlu 206
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Db 1217 GAA-----TCCATTTTACAGCAAGCTTACTGCTGTCAATGATCTTGGAGCTCTCT 1270
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Oy 207 SerlyeGlnleuGlnIIEHIsleuAspAspIIEValIIEProserAlaIIEValIIESer 226
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Db 1271 TCACCTTCATTCACATTCACATTTCTTGACATAGTGAGCTCTTCTCCGTCGGACAT 1330
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Oy 227 ArgAlaGlnIuThrIIEAsnAlaIIEThrValIIEProlyserThrIIEIleTYrTrpAspserGlnThr 246
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1331 AGAATCAAAATTTTCAAAAGCTTCGTGAGAGAGATGATACCTTTATGAGAGATGAGGA 1390
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 247 ThrIIEGluIuThrIIESerCyGlnMetArgTYrlysaIIEThrThraenGlnThrTrpAsn 266
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1391 CTGGTA-----CTGCTATTCAGCTCAGATATGCGCCAGTAAACAGAGCTTGGAAAT 1444
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 267 ValIIEGlnIuThrAspThrAsnPheThrTYrValIIE-----GlnGlnSerGluPheTYrLeu 284
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Db 1445 ATG-----GTATATTTACAAAGGCCAAAGAGACATGATTTGCTGATCTCG 1492

Oy 285 GIUProAsnIIElyeTYrValIIEPheGlnValIIEArgCysGln---GluThrGlylysaenTYr 303

Db 1493 AAACATTTACAGAAATATGAAATTTGAGATTTCTCTCAAGCTACATCTTATAAGGGAAGT 1552

Oy 304 TrpGlnProIIETrpSerProPhePheHIslyeThrProGluThrValIIEPro 320

Db 1553 TGGAGTATGAGATGATCAATTCATTCAGAGCAACCAACGAGAAAGAGCTT 1603

## RESULT 4

US-08-915-495-1  
 Sequence 1, Application US/08915495

Patent No. 5852176  
 GENERAL INFORMATION:

APPLICANT: Gubler, Ulrich A  
 TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESSES:  
 ADDRESSER: Hoffmann-La Roche Inc.

STREET: 340 Kingsland Street

CITY: Nucleiy

STATE: NO USA

COUNTRY: NO USA

ZIP: 07110

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/915,495

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/685,118

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Silverman, Robert A.  
 REGISTRATION NUMBER: 35,682

REFERENCE/DOCKET NUMBER: CD 9195

TELEPHONE: (201) 235-2863

TELEFAX: (201) 235-2363

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4040 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: CDNA

ANTI-SENSE: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 641..3226

US-08-915-495-1

## Alignment Scores:

pred. No.:	6.13e-13	Length:	4040
Score:	216.00	Matches:	75
Percent Similarity:	41.6%	Conservative:	57
Best Local Similarity:	23.7%	Mismatches:	131
Query Match:	6.5%	Indels:	54
DB:	2	Gaps:	13

US-10-667-289-2 (1-629) x US-08-915-495-1 (1-4040)

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Oy 32 GLVHIEIETRPVALGUPROALATRIIEPHELYMECGLYMEASNIIESEIETRY 51
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 731 GGGGATGTACTGTGAAGCTTCCCATGTATTTACTTGATCCACTGCATATTTACA 790
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  
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Qy 52 CyeglnalalaaleysaenCyeglnProaiglyleuhsiphetrylysaenglyile 71
Db 791 TGC-----TCCTTGAAGCCAGA----- 808
Qy 72 LyeGluarGpHeGlnleThraGlyleasnyThThralaargleuTPYrlysa--- 90
Db 809 CAAGGCTGCTTCACTATTCACAGCTAACAGTTA-----ATCCGTACAAAGTTT 859
Qy 91 -----AanPheleugluProHisaIa----- 97
Db 860 GACAGAAGATCAATTTTACCATGCGCACTCCCTCAATTCTCAAGTCACAGCTCTTCCC 919
Qy 98 -----SermetryrCyethralaGluCyProlyshisPheGlnluThrlau 113
Db 920 CTGGTACAACTTTGTTGTCGAAACTGGCCCTGT---ATCATATGATGAATAATTCAA 976
Qy 114 IleCyeglylysaPilleSerSerGlyTyTProProaspilleProaspGluValThrCys 133
Db 977 ATATGTGAGCAGAGATCTTGCTGGTGGTGGCTCCAGAACAGCTCAAAATTTATCTGTC 1036
Qy 134 ValIleTyGluTySerGlyAenMetThrCyethThThraHsaIa***LySleuThTyTyr 153
Db 1037 ATACAGAAGGAGAAGACAGGAGACTGTGCGCTGCACTGGGAAAGAGAGACGACACCCAC 1096
Qy 154 IleasPthrlyTyValIleValIleValIle-----LysSerleugluThThGluGlu 170
Db 1097 TTATACCTGAGTACTTACTTACAGCTTACAGTACCAAAATTTAATCTGACAGAACAA 1156
Qy 171 GlnGlnTyThrluThrsSerSerTyT-----LysanIleSerThrasPserleu 186
Db 1157 TGTAAGACATTTATTTGACTATTGTGAACTTTGGAATCAACCTCACCCCTGAACTCCT 1216
Qy 187 GlnGlylylylylylyTyThrluValITPValGlnIalaHsaIaIleuglymeGluGlu 206
Db 1217 GAA-----TCCATTTTACAGCCAGCAAGTTTACTCTCTCATATGCTTGAAGCTCCTCT 1270
Qy 207 SerlySglnleuglnIleHsaIleuaspIleValIleProSerIalaIleValIleSer 226
Db 1271 TCACCTTCATCCACATTCACATTCCTTGGACATATGAGGCTCTCTCCCTGGAGACATT 1330
Qy 227 ArgAlaGluThrlaIleasnaIaThValProlyThThrlleIleTyTThrasPserGlnThr 246
Db 1331 AGATCAAAATTTCAAAAGGCTCCGTGAGCAGATGTAACCTTTATTTGAGAGATGAGGGA 1390
Qy 247 ThrlleGluysValSerCySglnMeCArgTyThlysaIaThThrasGlnThThrasn 266
Db 1391 CTGGTA-----CTGCTTAATCGACTCAGATATGCGCCAGTAAACAGAGCTCTGGAAT 1444
Qy 267 VallySglnuPheasPthrAenPheThTyValIle-----GlnGlnSerGluPheTyThrlau 284
Db 1445 ATG-----GTTATGTTTACAAAGGCCAAAGAGACATGATTGCTGGAATCTG 1492
Qy 285 GlnProaspIleTyThValPheGlnValaArgCysGln--GluThrglylylysaTyTyr 303
Db 1493 AAACCATTTACAGAAATATGAAATTTCAAGATTCCTCTAAGTACATCTTTATTAAGGAAGT 1552
Qy 304 TTPGlnProTTPSerSerProPhePheHsaIeThThProGluThThValPro 320
Db 1553 TGGAGTATGAGTGAATGATCATTTGAGAGACAAACACAGAAAGAGAGCTT 1603

RESULT 5
US-08-914-520-1
; Sequence 1, Application US/08914520
; Patent No. 5919903
; GENERAL INFORMATION:
; APPLICANT: Gubler, Ulrich A
; APPLICANT: Preakey, David H
; TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
```

```
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/914,520
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,118
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Silverman, Robert A.
REGISTRATION NUMBER: 35,682
REFERENCE/DOCKET NUMBER: CD 9195
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-2863
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4040 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 641..3226
US-08-914-520-1

Alignment Scores:
Pred. No.: 6.13e-13 Length: 4040
Score: 216.00 Matches: 75
Percent Similarity: 41.6% Conservative: 57
Best Local Similarity: 23.7% Mismatches: 131
Query Match: 6.5% Indels: 54
DB: Gaps: 13

US-10-667-289-2 (1-629) x US-08-914-520-1 (1-4040)
Qy 32 GlyHiseIleTTPValGluProIaThThrllePheLyseGlyMeCAnIleSerIeTyTyr 51
Db 731 GCGAGTGTGACTGTGAAGCTTCCCATGTATTTACTTGGATCCACTGTCATATTTACA 790
Qy 52 CyeglnalalaaleysaenCyeglnProaiglyleuhsiphetrylysaenglyile 71
Db 791 TGC-----TCCTTGAAGCCAGA----- 808
Qy 72 LyeGluarGpHeGlnleThraGlyleasnyThThralaargleuTPYrlysa--- 90
Db 809 CAAGGCTGCTTCACTATTCACAGCTAACAGTTA-----ATCCGTACAAAGTTT 859
Qy 91 -----AanPheleugluProHisaIa----- 97
Db 860 GACAGAAGATCAATTTTACCATGCGCACTCCCTCAATTCTCAAGTCACAGGCTCTTCCC 919
Qy 98 -----SermetryrCyethralaGluCyProlyshisPheGlnluThrlau 113
Db 920 CTGGTACAACTTTGTTGTCGAAACTGGCCCTGT---ATCATATGATGAATAATTCAA 976
Qy 114 IleCyeglylysaPilleSerSerGlyTyTProProaspilleProaspGluValThrCys 133
Db 977 ATATGTGAGCAGAGATCTTGCTGGTGGTGGCTCCAGAACAGCTCAAAATTTATCTGTC 1036
Qy 134 ValIleTyGluTySerGlyAenMetThrCyethThThraHsaIa***LySleuThTyTyr 153
Db 1037 ATACAGAAGGAGAAGACAGGAGACTGTGCGCTGCACTGGGAAAGAGAGACGACACCCAC 1096
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/ TELEPHONE: 609-409-3035
/ TELEFAX: 413-254-9245
/ TELEEX: <Unknown>
/ INFORMATION FOR SEQ ID NO: 2897:
/ SEQUENCE CHARACTERISTICS:
/   LENGTH: 6019 base pairs
/   TYPE: nucleic acid
/   STRANDEDNESS: single
/   TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 2897:
US-09-543-679A-2897

Alignment Scores:
Pred. No.: 1,2e-12      Length: 6019
Score: 216.00          Matches: 75
Percent Similarity: 41.6%      Conservative: 57
Best Local Similarity: 23.7%   Mismatches: 131
Query Match: 6.5%           Indels: 54
DB: 5                     Gaps: 13

US-10-667-289-2 (1-629) x US-09-543-679A-2897 (1-6019)
QY 32 GlyHisIleTrpValGluProAlaThrIlePheMetGlyMetAlaSerIleTyr 51
Db 2710 GGGATGTGACTGGAAGCTTCCCATGTATTTTACTTGATCCACTGCAATATTACA 2769
QY 52 CyeglnAlaAlaIleLysAsnGlnProArgLysLeuHisPheTyrLysAenglyIle 71
Db 2770 TGC-----TCTTGAAGCCAGA----- 2787
QY 72 LysGluArgPheGlnIleThrArgIleAsnLysThrThrAlaArgLeuTyrTyrLys 90
Db 2788 CAAGGCTGCTTCACTATCCAGACGTACACAGTTA-----ATCCTGACCAAGTTT 2838
QY 91 -----AsnPheLeuGluProHisAla----- 97
Db 2839 GACAGAAAGATCAATTTTCAACCATGGCCACTCCCTCAATTCTCAAGTCACAGCTTCCC 2898
QY 98 -----SerMetTyrCysThrAlaGluCysProLysHisPheGlnGluThrLeu 113
Db 2899 CTTCGTACAACTTTGTCGTGCTGCAACTGGCCGT---ATCATATAGTAAATTCAA 2955
QY 114 IleCysGlyLysAspIleSerSerGlyTyrProProAspIleProAspGluValThrCys 133
Db 2956 ATATGTGAGAGAGAGATCTTCGTGTGTGCTCCACAAACGCTCAAAAATTATCTGCG 3015
QY 134 ValIleTyrGluTyrSerGlyAsnMetThrCysThrThrAsnAla***LysLeuThrTyr 153
Db 3016 ATACAGAAAGGAGAAACAGGAGACTGTGACCTGGACCTGGAAAGAGACAGACACCAC 3075
QY 154 IleAspThrLysTyrValValHisVal-----LysSerLeuGluThrGluGlu 170
Db 3076 TTATACCTGATGATCTACTCTACAGCTAAGTGAACCAAAAATTTAACTTGACGAGAACAA 3135
QY 171 GlnGlnTyrLeuThrSerSerTyr-----IleAsnIleSerThrAspSerLeu 186
Db 3136 TGTAAAGACATTATTTGCTGACTATTTGGAATTGGAATCAACCTCACCCCTGAATCACT 3195
QY 187 GlnGlyLysLysLysTyrLeuValTyrValGlnAlaAlaAsnAlaGluGlyMetGluGlu 206
Db 3196 GAA-----TCCAAATTACACAGCCAGAGTTACGCTGTCAATATCTTGAAGCTCTCT 3249
QY 207 SerLysGlnLeuGlnIleHisLeuAspAspIleValIleProSerAlaAlaValIleSer 226
Db 3250 TCACCTTCATCCACATTCACATTTCTTGACACATAGTAGGCTCTCTCCCTCGGGAACAT 3309
QY 227 ArgAlaGluThrIleAsnAlaThrValProLysThrIleIleTyrTrpAspSerGlnThr 246
Db 3310 AGATCAAAATTTCAAAGGCTTCGTCGAGACAGATGACCTTTATTTGAGAGAGAGAGGA 3369
QY 247 ThrIleGluLysValSerCysGluMetArgTyrTyrValAlaThrThrAsnGlnThrTrpAsn 266
Db 3370 CTGGTA-----CTGCTTAATCGACTGAGATATCGGCCAGATTACACAGCAGGCTCTGAAT 3423

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QY 267 ValIleGluPheAspThrAsnPhenTyrVal-----GlnGlnSerGluPheTyrLeu 284
Db 3424 ATG-----GTAAATGTTACAAAGGCCAAAGGAAGACATGATTTGCTGATCTG 3471
QY 285 GluProAsnIleLysTyrValPheGlnValArgCysGln---GluThrGlyLysArgTyr 303
Db 3472 AAACCATTTACAAATATGATGATTTCTCTTAAGCTACATCTTTATTAAGGAGAGT 3531
QY 304 TrpGlnProTyrSerSerProPheHisLeuThrProGluThrValPro 320
Db 3532 TCGAGTATTGGAGTGAATCATTCATGAGACACAAACACAGAAAGAGGCT 3582

RESULT 9
US-08-825-558-5
/ Sequence 5, Application US/0882558
/ Patent No. 5965724
/ GENERAL INFORMATION:
/ APPLICANT: SHARKEY, ANDREW
/ APPLICANT: SMITH, STEPHEN K.
/ APPLICANT: DELLOW, KIMBERLEY A.
/ TITLE OF INVENTION: GP 130 Lacking the Transmembrane Domain
/ NUMBER OF SEQUENCES: 14
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
/ STREET: 1100 NEW YORK AVENUE
/ CITY: WASHINGTON
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/825,558
/ FILING DATE: 19-MAR-1997
/ CLASSIFICATION: 536
/ ATTORNEY/AGENT INFORMATION:
/ NAME: ESMOND, ROBERT W.
/ REGISTRATION NUMBER: 32,893
/ REFERENCE/DOCKET NUMBER: 0623.0530001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)371-2600
/ TELEFAX: (202)371-2540
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/   LENGTH: 2754 base pairs
/   TYPE: nucleic acid
/   STRANDEDNESS: both
/   TOPOLOGY: linear
/   MOLECULE TYPE: cDNA
/ FEATURE:
/   NAME/KEY: CDS
/   LOCATION: 1..2754
/ US-08-825-558-5

Alignment Scores:
Pred. No.: 1.16e-12      Length: 2754
Score: 211.00          Matches: 172
Percent Similarity: 32.7%      Conservative: 118
Best Local Similarity: 19.4%   Mismatches: 276
Query Match: 6.3%           Indels: 320
DB: 2                     Gaps: 44

US-10-667-289-2 (1-629) x US-08-825-558-5 (1-2754)
QY 4 ValThrIleGlnTrpAspAlaValIleAlaLeuTyrIleuPheSerTrpCysHisGly 23
Db 4 TTGACGTGACAGCTTCGGAGTGCAGAGCTTTTATTTTCTGACCACTGATATACA 63
QY 24 GlyIleThrAsnIleAsnGlnLysSerGlyHisIleTyrValGluProAlaThrIlePheLys 43

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Db      64  GGTAAGTCTAGATCATGT---GGTATATCATGCTCTGAA---TCTCAGATTGACAA 117
Qy      44  MetGlyMetSerHisSerIleTyrCysGlnAlaIleIysAsnGly 63
Db      118  CTTCATTCTTAATTCATGCAAGTTTGT-----GTCTAAAGAAAAAATGATGATTAT 171
Qy      64  LeuHisPheTyrIysAsnGlyLe-----LysGlu 73
Db      172  TTTCAGTAATAGCTAATTAATTCATGCTGCAAAAACCAATTTTACTATTCCTTAAGAG 231
Qy      74  ArgPheGlnIleThrArgIleAsnIysThrAlaArgLeuTyrIysAsnPheLeu 93
Db      232  CAATATCACTATC-----ATAACAGAACAGACATCCAGTGTCACTTACAGATATAGCT 285
Qy      94  GluProHisAlaSerMetTyrCysThrAlaGluCysProIysHisPheGlnIleu 113
Db      286  TCATTAATATTCAGCTCCTGACATTCCTTAATTCGAGACAGCTTGAACAGAAAT--- 342
Qy      114  IleCysGlyIysAsnIleSerSerGlyTyrProProAsnIleProAsnGluValThrCys 133
Db      343  GTTTATGGAATTCACATTAATTTGAGCTTGCCTCCAGAAAACTTAATAATTTGAGTTGC 402
Qy      134  ValIleTyrGluTyrSerGlyAsnMetThrCysThrTyrAsnAla**LysLeuThrTyr 153
Db      403  ATGTGAAACAG---GGAGAAAGAAATGAGTGTGAGTGGATGGTGAAGGAAACACAC 459
Qy      154  IleAspThrIysTyrValValHis----- 161
Db      460  TTGAGACAAACTTCACTTAAATATGAAATGGCAACACAAAGTTTGTCTGATTCGAA 519
Qy      162  ---ValIysSerLeuGluTyrGluGluGlnIleThrLeuThrSerSerTyrIleAsn 180
Db      520  GCAAAAGTACACCCACCCTCATGCACTGTGATTAATTCATGCTGTAATTTGTGTAAC 579
Qy      181  IleSerThrAspSerLeuGlnIylGlyIysLeuValTyrValGlnAlaIleAsn 200
Db      580  ATTGAA-----CTCTGGTGAAGACAGAAAT 606
Qy      201  AlaLeuGlyMetGluSerIysGlnLeuGlnIleHisLeuAspAspIleVal----- 218
Db      607  GCCCTGGGAAGGTTACATCAGAT-----CATATCAATTTGATCCTGTATATTAAGTG 660
Qy      219  ---IleProSerAlaIleValIleSerArgAlaGluThrIleAsnAlaThrVal 235
Db      661  AAGCCCAATCCGACATAATTTATGATCACTCAACTCAGAGAAAGCTGTAGATCTTA 720
Qy      236  ProIysThrIleIleTyrTyrAspSerGlnThr-----ThrIleGlyIysValSerCys 253
Db      721  AATTGACA-----TGGACCAACCCAGATTAAGAGTGTATTAATTAATAATAT 771
Qy      254  GluMetArgTyrIysAlaThrThrAsnGlnThrTyrAsn---ValIysGluPheAspThr 272
Db      772  AACTTCATATATAGAACCAAGATGCTCAACTTGGAGCCAGATTCCTCTCGAAGACACA 831
Qy      273  AsnPheThrTyrValGlnGlnSerGluPheTyrLeuGluProAsnIleIysTyrValPhe 292
Db      832  GCATCCACCCGATCTTCATTCACGTGCCAAGACCTTAACCTTTTACAGAAATATGTTT 891
Qy      293  GlnValArgCys---GlnGluThrGlyIysArgTyrTyrGlnIleProIlePheSerSer----- 309
Db      892  AGGATTCGCTGTATGAAGAAAGATGTTAAGGATACCTGAGTACTGAGATGAAGAAACA 951
Qy      310  ---ProPhePheHisIysThrPro 316
Db      952  AGTGGATCACTATGAAAGATAGACATTAAGACCAAGCAAGTTTCTGTGTAAATAATAGAT 1011
Qy      317  ---GluThrValPro----- 320
Db      1012  CCATCCCATACTCAAGGCTACAGAACTGTACAACTCGTGTGAAGACATTTGCCCTTTT 1071
Qy      321  GlnValThrSerIysAlaPheGlnHisAspThr-----TyrAsnSerGlyLeu 336

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Db      1072  GAAGCAATGAGAAAAATCTTGATTAATGAAGTCTCTCAAGATGAGAAATCACTTA 1131
Qy      337  ---ThrVal---AlaSerIleSerThrGlyHisLeuThrSerAspAsnArgGly 352
Db      1132  CAAAATTACACAGTTAATGCCACAAAACAGCAGTAATTAATTCACAAATGATGCC----- 1185
Qy      353  AspIleGlyLeuLeuLeuGlyMetIleValPheAlaValMetLeuSerIleLeuSerLeu 372
Db      1186  ---TATCTGAACACCTTAACAGTAAGAAATCTT 1215
Qy      373  IleGlyIlePheAsn----- 377
Db      1216  GTTGGCAAAATCAGATCAGCTGTTTAATTAATCCCTGCTGATGATCTTCAAGCTACAC 1275
Qy      378  ---ArgSerPhe----- 380
Db      1276  CCTGTATGATGATCTTAAGATATTCACCCAAAGATTAACATGCTTTGGGTGCAATGATACT 1335
Qy      381  ---ArgThrGlyIleIysArgArgIleLeuLeuIleProIysTyrLeuTyrGluAsp 399
Db      1336  CCAAGGGAATCTGTAAAGAAATATATCTT-----GAGTGTGT----- 1374
Qy      400  IleProAsnMetIysAsnSerAsnValValIysMetLeuGlnIleAsnSerGluLeu--- 418
Db      1375  GTGTATCAGATTAAGACACCTGTATCAGACACTGCAACAGAAAGATGATACCGTGCAT 1434
Qy      419  ---MetAsnAsnAsnSerSerGluGlnIleValLeuTyr-----ValAspPro 432
Db      1435  CGCACTATTTTAAGAGGAACCTTAGAGAGAAATGCTATTTGATTAACAGTTACTCCA 1494
Qy      433  MetIleThrGlu-----IleIysGluIlePhe 441
Db      1495  GTATATGCTGATGACACAGGAACCTGAAATCATTAAGCATACCTTAACAGACT--- 1551
Qy      442  IleProGluHisIysProThrAspTyrIysIys-----GluAsnThrGlyProLeu 458
Db      1552  CCACCTTCCAAAGACACTTCTGTGTCGACCAAAAAGTAGGAAAAAGAAAGCTGTCTTA 1611
Qy      459  GluThrArgAspTyrPro-----GluAsnSerLeuPheAsnThrThrValVal 475
Db      1612  GAGTGGACCAACTCTGTGATGTTCAAGAAATGATTATACAAATATTAATTAATTT 1671
Qy      476  Tyr----- 476
Db      1672  TATGAACCATCATTTGGAATGAAGAACTGCTGTGAATGTGATTTCTCCACACAGAAATAT 1731
Qy      476  --- 476
Db      1732  ACATGTCCTCTTACTAGTACATGATGATGATGATGATGATGATGATGATGATGATGAT 1791
Qy      476  --- 476
Db      1792  GAAGTGGAGAGATGTCAGAAATTCATCTTAACTCCCAAGTTTGTCTCAAGAGAA 1851
Qy      476  --- 476
Db      1852  ATTGAAGCAATAGTGTGCTGTGCTTGAATTCCTATTAAGCAACTCTTCTGGAGTG 1911
Qy      477  ---IleProAsp 479
Db      1912  CTGTCTGCTTAAATGAAGACACTAATTAATAAACACATCTGCGCTAATGCTCAGAT 1971
Qy      480  LeuAsnThrGlyTyrIysProGlnIleSer-----AsnPheLeu 492
Db      1972  CTTCAAGAGTATATATGCGCCAGTGTCACTCACAATCTCCAAAGCAATTTTAAT 2031
Qy      493  ProGluGlySerHisLeuSerAsnAsn-----GluIleThr 505
Db      2032  TCAAAAGATCAATATGATTAATGAGTCAATTTCACTGATGATAGTGTGTGAAATAGAA 2091
Qy      506  SerLeuThrLeuIysPro---ProValAsp---SerLeuAsp----- 517
Db      2092  GCAAAAGACAAAAGCCTTTTCCAGAAAGATCTGAATTCATTTGACCTGTTCAAAAGAA 2151

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Qy 518 -----SerGlyAsnAsnProArgLeuGlnIys 526
Db 2152 AAAATTAATCTGAAGACACAGACAGTGTATTGGGGGGCTTCATGTCATGTCATCTTCT 2211
Qy 527 HisProAsnPheAlaPheSerValSerSerValAsnSerLeuSerThrIlePheLeu 546
Db 2212 AGCCCAAGCATTTCTAGCAGTGAATAATGAACTTCA---CAAAACCTCGACGACT 2268
Qy 547 GlyGluSerLeuIleLeuAsnGlnGly---GluCysSerSerProApIleGln--- 564
Db 2269 GTCCAGATTCTACCGGTGACACAGTGGCTACACACCAAGTTCCTGTCAGTCCAGTCTC 2328
Qy 565 AsnSerValGluGluGluThrThrMetLeuLeuGluAsnAspSerProSerGluThrIle 584
Db 2329 TTCTCAAGATCCGAGCTCTACCCAGCCTTGTATGAT-----TCAGAGAGACGG 2376
Qy 585 ProGluGlnThrLeuLeuProAspGluPheValSerCysLeuGlyIleValAsnGluGlu 604
Db 2377 CCAGAACATCTACATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2436
Qy 605 LeuProSerIleAsnThrTyPheProGluAsnIleLeuGlu----- 618
Db 2437 -----CAGTACTTCAACAGAACTGCGATCGATCGATCGATCGATCGATCGAT 2481
Qy 619 ---SerHisPheAsnArg 623
Db 2482 ATTTCACTTTTGAAGG 2499

RESULT 10
US-09-312-611-5
; Sequence 5, Application US/09312611
; Patent No. 6380160
; GENERAL INFORMATION:
; APPLICANT: SHARKEY, ANDREW
; APPLICANT: SMITH, STEPHEN K.
; APPLICANT: DELLOW, KIMBERLEY A.
; TITLE OF INVENTION: Gp130 Lacking the Transmembrane Domain
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/312.611
; FILING DATE: 17-MAY-1999
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0623.0530002
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2754 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2754
; US-09-312-611-5

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Alignment Scores:
Pred. No.: 1,16e-12 Length: 2754
Score: 211.00 Matches: 172
Percent Similarity: 32.7% Conservative: 118
Best Local Similarity: 19.4% Mismatches: 276
Query Match: 6.3% Indels: 320
DB: 3 Gaps: 44

US-10-667-289-2 (1-629) x US-09-312-611-5 (1-2754)
Qy 4 ValThrIleGlnThrAspAlaValIleAlaLeuTyIleLeuPheSerTrpCysHisGly 23
Db 4 TTACACCTTCACAGCTTGAGTGAAGCAAGCTGTATTATTTCTCTACCACTGAATCTACA 63
Qy 24 GlyIleThrAsnIleAsnCysSerGlyHisIleTrpValGluProAlaThrIlePheIys 43
Db 64 GGTGAACCTCTAGATCCATGT---GGTTATATAGTCCGAA---TCTCAGATTGACAA 117
Qy 44 MetGlyMetAsnIleSerIleTyCysGlnAlaAlaIleLysAsnCysGlnProArgIys 63
Db 118 CTTCATTTCAATTTCACTGACGATTTGT-----GTCTAAAGGAAAAATGATGATTAT 171
Qy 64 LeuHisPheTyIleAsnGlyIle----- 73
Db 172 TTTCATGTAAATGCTAAATTAATTAATGATGTAAGAAACCAACATTACTATTCCTAAGAG 231
Qy 74 ArgPheGlnIleThrArgIleAsnLysThrThrAlaArgLeuTrpTyIleAsnPheLeu 93
Db 232 CAATATATCTATC-----ATAAACAGACAGCATCCAGTGTCACTTACAGATATAGCT 285
Qy 94 GluProHisLeuSerMetTyCysThrAlaGluCysProLysHisPheGlnGluThrLeu 113
Db 286 TCATTAATATTGAGCTACCTTCAACATTTCTACATTCGACAGCTGAACAGAAAT--- 342
Qy 114 IleCysGlyLysAspIleSerSerGlyTyProProAspIleProAspGluValThrCys 133
Db 343 GTTTATGATGATCAACAATTAATTTCAAGCTTCCCTCCAGAAAACCTAAATTTGAGATTGC 402
Qy 134 ValIleTyGluLysSerGlyAsnMetThrCysThrTrpAsnAla**LysLeuThrTy 153
Db 403 ATGTGAACAG---GGAAAGAAATAGAGTGAAGTGAAGTGAAGGAAACACAC 459
Qy 154 IleAspThrLysTyValValHis----- 161
Db 460 TTGAGACAAACTTCACTTAATAAATCGAATGGCAACACAAAGTTGCTGATGCAAA 519
Qy 162 ---ValLysSerLeuGluThrGluGluGlnGlnGlnIleuThrSerSerTyIleAsn 180
Db 520 GCAAAACGTGACACCCCACTTCATGACATGTTGATTATTTACTGTGTATTTGTCAAC 579
Qy 181 IleSerThrAspSerLeuGlnGlyLysTyLeuValTrpValGlnAlaIleAsn 200
Db 580 ATTGAA-----GCTGGGTGAAGCAGAGAAAT 606
Qy 201 AlaLeuGlyMetGluGluSerLysGlnLeuGlnIleHisLeuAspAlaIleVal----- 218
Db 607 GCCCTTGGGAAGTTACATCAGAT-----CATATCAATTTGATCTGTATTAAGAAG 660
Qy 219 -----IleProSerAlaAlaValIleSerArgAlaGluThrIleAsnAlaThrVal 225
Db 661 AAGCCCAATCCGACATATTAATTAATGATGATCAATGATCAAGAGAACTGTCTATATCTTA 720
Qy 236 ProLysThrIleIleTyTrpAspSerGlnThr-----ThrIleGluLysValSerCys 253
Db 721 AAATGACA-----TGACCAACCCCAAGATTAAGAGTGTATTAATCTAAATAAT 771
Qy 254 GluMetArgTyIleValAlaThrThrAsnGlnThrTrpAsn---ValLysGluPheAspThr 272
Db 772 AACATTCATATAGACAAAGATGCTCAACTTGAGCGCAATTCCTCTGAAGACACA 831
Qy 273 AsnPheThrTyValGlnGlnSerGluPheTyLeuGluProAsnIleLysTyValPhe 292

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Db 832 GCATCCACCCGATCTTCATTCATGTCGCAAGACCTTAACCTTTTACAGAAATATGTTT 891  
 Qy 293 GlnValArgCys---GlnGluThrGlyLeuArgPheThrProTyrPheProTyrPheSer----- 309  
 Db 892 AGGATTCGCTGATGATGAGAAAGATGTAAAGGATACGTAGAGTACCTGAGTGAAGAACCA 951  
 Qy 310 -----ProPhePheHisLeuThrPro 316  
 Db 952 AGTGGGATCACTATGAAGATAGACCATTAAGACCAAGTTTCTGTTATTAATAATGAT 1011  
 Qy 317 -----GluThrValPro----- 320  
 Db 1012 CCATCCCATCTCAGAGCTACAGAACTGTACAACCTCGTGTGAGAGACATTTGCCCTCTTTT 1071  
 Qy 321 GlnValThrSerLeuValPheGlnHisAspThr-----TrpAsnSerGlyLeu 336  
 Db 1072 GAAGCCCAATGAAAATCTTGATTAATGATGACCTTCACACAGATGAAATTCACATTTA 1131  
 Qy 337 -----ThrVal---AlaSerIleSerThrGlyHisLeuThrSerAspAsnArgGly 352  
 Db 1132 CAATAATTCACAGTATATGCGACAAACCTGACAGTAATCTTCACAAATGATCGC----- 1185  
 Qy 353 AspIleGlyLeuLeuLeuGlyMetIleValPheAlaValMetLeuSerIleLeuSerLeu 372  
 Db 1186 -----TATCTAGCAACCTTAACAGTAAAGAAATCTT 1215  
 Qy 373 IleGlyIlePheAsn----- 377  
 Db 1216 GTTGGCAATCAATGACAGCTGTTTAACTATCCCTGCTGTGACCTTCAAGCTACAC 1275  
 Qy 378 -----ArgSerPhe----- 380  
 Db 1276 CCTGATATGATCTTAAAGCATTCCTCCAAAGATTAACATGCTTGGGTGGAATGACACT 1335  
 Qy 381 ---ArgThrGlyIleLeuArgArgIleLeuLeuLeuIleProIlePheLeuThrGlyAsp 399  
 Db 1336 CCAAGGGAATCTGTAAAGAAATATATCTT-----GAGTGTGT----- 1374  
 Qy 400 IleProAsnMetLeuAsnSerAsnValValIleMetLeuGlnIleAsnSerGlyLeu--- 418  
 Db 1375 GTGTTATGACATTAAGACCCCTGTATCAGACATGCGACAGAAAGATGATCGTGCAT 1434  
 Qy 419 -----MetAsnAsnAsnSerSerGlyGlnValLeuThr-----ValAspPro 432  
 Db 1435 CGCACCTATTTAAGAGGAACTTAGCAGAGAGCAAAATGCTATTGATTAACAGTTACTCCA 1494  
 Qy 433 MetIleThrGlu-----IleLeuGlnIlePhe 441  
 Db 1495 GTATATGCTGATGAGACCAAGAGCCCTGATCCATTAAGCATTAACAAGCT--- 1551  
 Qy 442 IleProGlnHisLeuPheProThrAspIleLeuLeu-----GluAsnThrGlyProLeu 458  
 Db 1552 CCACCTTCCAAAGACCTACTGTGCGACAAAAAAGTAGGAAAAAGCAAGCTGTCTTA 1611  
 Qy 459 GlnThrArgAspIlePro-----GlnAsnSerLeuPheAsnThrValVal 475  
 Db 1612 GAGTGGGACCAACTTCTGTGTGATGTTCAAAATGATTTATCAAAATTTATCTATATTT 1671  
 Qy 476 Tyr----- 476  
 Db 1672 TATAGAACCATCATTTGGAATAAAGCTGTGAAATGTGATTTCTTCCACAGAAATAT 1731  
 Qy 476 ----- 476  
 Db 1732 ACATTTCTCTTTGACTAGTACACATTTGACATGTTGACAAATGCGACAGATCAAGAT 1791  
 Qy 476 ----- 476  
 Db 1792 GAAGGTGGGAAGATGTCCAGAAATTCATTTTACTACCCCAAGTTTGTCAAGAGAA 1851  
 Qy 476 ----- 476  
 Db 1852 ATTGAAGCATATAGTCGTGCTGTTGCTTAGCATTTCTATTTGACAACTTCTGTGGAGTG 1911

Qy 477 -----IleProAsp 479  
 Db 1912 CTGTTCTGCTTAATAAGCAGACCTTAATTAATAACATCTGGCTTAATGTTCCAGAT 1971  
 Qy 480 LeuAsnThrGlyThrLeuProGlnIleSer-----AsnPheLeu 492  
 Db 1972 CTTCAAAAGATCATATTTGCCAGTGTCACTCACACTCTCCCAAGCACAATTTAAT 2031  
 Qy 493 ProGlnIleSerIleLeuSerAsnAsn-----GluIleThr 505  
 Db 2032 TCAAAAGATCAAAATGATTTAGATGCGAATTTCACTGATTAAGTTGTGGAAATAGAA 2091  
 Qy 506 SerLeuThrLeuLeuPro---ProValAsp-----SerLeuAsp----- 517  
 Db 2092 GCAAAATGACAAAAGCTTTTCCAGAAATCTGAATCATTTGACCTGTTCAAAAAGAA 2151  
 Qy 518 -----SerGlyAsnAsnProArgLeuGlnLeu 526  
 Db 2152 AAATTAATTAAGAGACACAGCAGTGTGATTTGGGGGTCTTCATGATCATGTCATCTTCT 2211  
 Qy 527 HisProAsnPheAlaPheSerValSerSerValAsnSerLeuSerAsnThrIlePheLeu 546  
 Db 2212 AGGCCAAGCATTTCTAGCAGTGAATAATGAAATCTTCA---CAAAACACTTGCAGACT 2268  
 Qy 547 GlyIleLeuSerLeuIleLeuAsnGlnGly---GlyCysSerSerProAspIleGln--- 564  
 Db 2269 GTCCAGATTTCTACCGTGTACACAGTGTGCTACAGACACCAAGTCCGTGATCCAAATC 2328  
 Qy 565 AsnSerValGlnGluGluThrThrMetLeuLeuGlnAsnAspSerProSerGluThrIle 584  
 Db 2329 TTCTCAAGATCCGAGCTACCCAGCCCTGTTGAT-----TCAGAGAGACGG 2376  
 Qy 585 ProGlnGlnThrLeuLeuProAspGluPheValSerCysLeuGlyIleValAsnGlnGlu 604  
 Db 2377 CCAGAAATCTACAAATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2436  
 Qy 605 LeuProSerIleAsnThrThrPheProGlnAsnIleLeuGlu----- 618  
 Db 2437 -----CAGTACTTCAACAGACACTGACATGACATGATCCATCCAGAT 2481  
 Qy 619 ---SerHisPheAsnArg 623  
 Db 2482 ATTTCACATTTGAAAG 2499  
 RESULT 11  
 US-09-023-655-1131  
 ; Sequence 1131, Application US/09023655  
 ; Patent No. 6607879  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cocks, Benjamin G.  
 ; APPLICANT: Susan G. Stuart  
 ; APPLICANT: Jeffrey J. Sellhammer  
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
 ; TITLE OF INVENTION: EXPRESSION  
 ; NUMBER OF SEQUENCES: 1508  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
 ; STREET: 3174 PORTER DRIVE  
 ; CITY: PALO ALTO  
 ; STATE: CALIFORNIA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
 ; CURRENT APPLICATION DATA:  
 ; FILING DATE: US/09/023, 655  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:

APPLICATION NUMBER:  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Zeller, Karen J.  
 REGISTRATION NUMBER: 37,071  
 REFERENCE/DOCKET NUMBER: PA-0001 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 855-0555  
 TELEFAX: (650) 845-4166  
 INFORMATION FOR SEQ ID NO: 1131:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3085 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: GENBANK  
 CLONE: g186353  
 US-09-023-655-1131

## Alignment Scores:

Pred. No.:	2,35e-12	Length:	3085
Score:	209.00	Matches:	172
Percent Similarity:	32.7%	Conservative:	118
Best Local Similarity:	19.4%	Mismatches:	276
Query Match:	6.3%	Indels:	320
		Gaps:	44

US-10-667-289-2 (1-629) x US-09-023-655-1131 (1-3085)

QY 4 ValThrIleGlnTrpAspAlaValIleAlaLeuTyrIleLeuPheSerTrpCysHisGly 23  
 Db 259 TTGACGTGGACGAGCTGGGTAGTCAGACCTGTTTATTTCCACACAGTAATTCACA 318  
 QY 24 GlyIleThrAsnIleAsnCysSerGlyHisIleTrpValGluProAlaThrIlePheLys 43  
 Db 319 GGTAACTTCAGATCCATGT---GGTTATATCAGTCTGAA---TCGCCAGTTGTCAA 372  
 QY 44 MetGlyMetAsnIleSerIleTyrCysGluAlaAlaIleLysAsnGlnProArgLys 63  
 Db 373 CTTATCTTAATTTTCATGCGCAGTTGT-----GTCTAAAGAAAAATGATGATAT 426  
 QY 64 LeuHisPheTyrIlyAsnGlyIle-----LysGlu 73  
 Db 427 TTTCATGTAATGCTAATTAATTCATTGTCGAAACAAACATTTTACTATTCCTAAAGAG 486  
 QY 74 ArgPheGlnIleThrArgIleAsnLysThrAlaArgLeuTrpTyrLysAsnPheLeu 93  
 Db 487 CAATATATCTATC-----ATTAACGAAACAGCATCCAGTGCACCTTACAGATATGCT 540  
 QY 94 GluProHisAlaSerMetTyrCysThrAlaGluCysProLysHisPheGlnIleu 113  
 Db 541 TCATTAATATTCAGCTCAGCTCAGCAACATTTCAATTCGACAGCTTGAACAGAT--- 597  
 QY 114 IleCysGlyLysAspIleSerSerGlyTyrTrpProAspIleProAspGluValThrCys 133  
 Db 598 GTTATGGAATCAACAATATTTCAAGCTGCTCCAGAAAAAATTTAAATTTGAGTTGC 657  
 QY 134 ValIleTyrGluTyrSerGlyAsnMetThrCysThrTrpAsnAla---LysLeuThrTyr 153  
 Db 658 ATTGTGAACGAG---GGGAAGAAATAGAGGTGAGTGGATGGAGAGGAAACACAC 714  
 QY 154 IleAspThrLysTyrValIleHis-----LysPro 161  
 Db 715 TTGAGAGCAAACTTCATTAATAATCGAATGGGCAACACAAAGTTTGCATTCGAA 774  
 QY 162 ---ValLysSerLeuGluThrGluGluGluGlnIleuTyrLeuThrSerSerTyrIleAsn 180  
 Db 775 GCAAAAGGTGACACCCACCTCAGCACTGTGATTAATTCATCGTGTATTTGTGCAC 834  
 QY 181 IleSerThrAspSerLeuGlnGlyLysLysTyrLeuValIleProValGlnAlaAsn 200

Db 835 ATGGA-----GTCTGGGTAGAGCAGAGAT 861  
 QY 201 AlaLeuGlyMetGluSerLysGlnLeuGlnIleHisLeuAspPheIleVal----- 218  
 Db 862 GCCCTTGGGAAGTTTACATCAGAT-----CATTCATATTTGATCCTGTATTAAGTG 915  
 QY 219 -----IleProSerAlaAlaValIleSerArgAlaGluThrIleAsnAlaThrVal 235  
 Db 916 AACCCCAATCCGCACATTAATTTATGATGATCACTCAAGAGCACTGTCTAGATCTTA 975  
 QY 236 ProLysThrIleIleTyrTrpAspSerGlnThr-----ThrIleGluLysValSerCys 253  
 Db 976 AAATTGACA-----TGACCAACCCAGATTAAGAGTGTATTAATTAACATAAT 1026  
 QY 254 GluMetArgTyrLysAlaThrThrAsnGlnThrTrpAsn---ValLysGluPheAspThr 272  
 Db 1027 AACATTCAATTAAGACCAAAAGATGCTCACTTGAGAGCAAGATCTCCTGAAGACACA 1086  
 QY 273 AsnPheThrTyrValGlnGlnSerGluPheTyrLeuGluProAsnIleLysTyrValPhe 292  
 Db 1087 GCATCCACCCGATCTTCATTCATGCTGCCAAGACCTTAACCTTTTACAGAAATGTGTT 1146  
 QY 293 GlnValArgCys---GlnGluThrGlyLysArgTyrTrpGlnProTrpSerSer----- 309  
 Db 1147 AGGATTCGCTGTATGAAGAAAGATGTGAAGATACCTGAGTGAAGTGAAGAGCA 1206  
 QY 310 -----ProPhePheIleLysThrPro 316  
 Db 1207 AGTGGATCACCTATGAAGATAGACCATTAAGACCAAGTTTCTGGTATTAATAGAT 1266  
 QY 317 -----GluThrValPro----- 320  
 Db 1267 CCATCCCATCTCAAGCTACAGAACTGTCAACCTGTGTGAAGACATGCTCCTTTT 1326  
 QY 321 GlnValThrSerLysAlaPheGlnHisAspThr-----TrpAsnSerGlyLeu 336  
 Db 1327 GAAGCCAAATGGAATAATCTTGATTAAGAGTGAAGTCTCAAGATGAAGAAATCATTTA 1386  
 QY 337 -----ThrVal---AlaSerIleSerThrGlyHisLeuThrSerAspAsnArgGly 352  
 Db 1387 CAAAATTAACAGATTATGTCACAAACAGACGTAATCTTCAAAATGATGCC----- 1440  
 QY 353 AspIleGlyLeuLeuGlnMetIleValPheAlaValMetLeuSerIleLeuSerLeu 372  
 Db 1441 -----TATCTAGCAACCTTACAGTAAGAAATCTT 1470  
 QY 373 IleGlyIlePheAsn----- 377  
 Db 1471 GTTGGCAAAATCAGATGCAAGCTGTTTAATCTATCCCTGCTGTGACTTCAAGCTACTCAC 1530  
 QY 378 -----ArgSerPhe----- 380  
 Db 1531 CCGTATATGATCTTAAAGATTCGCCAAAGATTAACATGCTTGGGTGGATGAAGACTACT 1590  
 QY 381 ---ArgThrGlyIleLysArgArgIleLeuLeuLeuIleProLysTrpLeuTyrGluAsp 399  
 Db 1591 CCAAGGGAATCTGTAAAGAAATATATATCTT-----GAGTGGTGT----- 1629  
 QY 400 IleProAsnMetLysAsnSerIleAsnValIleLysMetLeuGlnIleAsnSerGluLeu--- 418  
 Db 1630 GTGTATTCAGATTAAGACCCCTGTATTCACAGACTGGCAACAGAAAGATGTACCGTGCAT 1689  
 QY 419 -----MetAsnAsnAsnSerSerGluGlnValLeuTyr-----ValAspPro 432  
 Db 1690 CGCACCTATTAAGAGGAAGCTTAGACAGAGAGCAAAATGCTATTTGATTAACAGTACTCCA 1749  
 QY 433 MetIleThrGlu-----IleLysGluIlePhe 441  
 Db 1750 GTATATGCTGATGACAGAGAACCTGATATCATTAAGCATTAACAAAGCT--- 1806  
 QY 442 IleProGlnHisLysProThrAspTyrLysLys-----GluAsnThrGlyProLeu 458  
 Db 1807 CCACCTTCCAAAGGACCTACTGTTCGACCAAAAAAGTAGGAAAAAGAACTGTCTCTTA 1866



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Db      916 AACCCACCGCCACATTAATTATCATCACTGATCAACAGAGAACTGTATGATCTTA 975
Qy      236 ProlyserThrIleIleTyrTrpAspSerGlnThr-----ThrIleGluValSerCys 253
Db      976 AAATTGACA-----TGACCACACCAAGTATTGAAGTGTATTAAATCTTAAATAT 1026
Qy      254 GluMetArgTyrIleValThrThrAsnGlnThrTrpAsn---ValIleGluPheAspThr 272
Db      1027 AACATTCAATATAGACCAAAAGATGCTCAACTGGAGCAGATCTCTCTGAAAGACACA 1086
Qy      273 AsnPheThrTyrValGlnGlnSerGluPheTyrLeuGluProAsnIleIleTyrValPhe 292
Db      1087 GCATCCACCCGATCTTCATTCACCTGTCMAAGACCTTAACCTTTTACAGAAATAGTGT 1146
Qy      293 GlnValArgCys---GlnGluThrGlyLeuArgTyrTrpGlnProIlePheSerSer----- 309
Db      1147 AGGATTGCTGTATGAAGAAAGATGTGAAGATACCTGAGTACTGATGAAGAAAGCA 1206
Qy      310 -----ProPhePheIleIleTyrThrPro 316
Db      1207 AGTGGATCATCATGAAGATAGACCATTAAGACCAAGTTCTGTATTAATAATAGAT 1266
Qy      317 -----GluThrValPro----- 320
Db      1267 CCATCCCATATCAAGGCTACAGAACTGTACAACCTGTGTGAAGACATTCCTCTTTT 1326
Qy      321 GlnValThrSerIleValPheGlnIleAspThr-----TrpAsnSerGlyLeu 336
Db      1327 GAAGCCAAATGAAAATCTTGATTAATGAAGTACTCAACAAGATGAATGCAATTTA 1386
Qy      337 -----ThrVal---AlaSerIleSerThrGlyIleValIleThrSerAspAsnArgGly 352
Db      1387 CAAAATTACACAGTTAATGCCACAAACTGACAGTAATATCTCAAAATGATGCG----- 1440
Qy      353 AspIleIleIleuLeuGluMetIleValPheIleValIleMetLeuSerIleLeuSerLeu 372
Db      1441 -----TATCTACCAACCTTACAGTAAGTAAGAAATCTT 1470
Qy      373 IleGlyIlePheAsn----- 377
Db      1471 GTTGCAAAATCAAGATGACGCTTTTAACTATCCCTGCTGTGACTTCAAGCTACAC 1530
Qy      378 -----ArgSerPhe----- 380
Db      1531 CCTGTATGATCTTAAGACATTCCTCAAGATTAACATGCTTGTGGTGAATGGAATCT 1590
Qy      381 ---ArgThrGlyIleIleValArgIleIleLeuLeuIleProIleTyrGluAsp 399
Db      1591 CCAAGGGAATCTGTAAAGAAATATATACTT-----GAGTGTGT----- 1629
Qy      400 IleProAsnMetIleAsnSerAsnValIleValIleMetLeuGlnIleAsnSerGluLeu 418
Db      1630 GTGTATCAAGATTAAGACCTGTATCAACAGACTGCGCAACAGAAAGATGTAACCTG 1689
Qy      419 -----MetAsnAsnSerSerGluGlnValIleTyr-----ValAspPro 432
Db      1690 CGCAGCTATTAAGAGGAACTTAGCAGAGAGCAATGCTATTTGATTAACGTTATCCA 1749
Qy      433 MetIleThrIle----- 441
Db      1750 GTATATGCTATGATGACAGAGAGCCCTGAATCCATTAAGGATACCTTTAAACAAGCT 1806
Qy      442 IleProGluIleIleValProThrAspTyrIleIleIle-----GluAsnThrGlyProLeu 458
Db      1807 CCACCTTCCAAAGACCTACTGTTCCGACAAATAAGTGAAGAAAAAGAGAGCTGCTT 1866
Qy      459 GluThrArgAspTyrPro-----GluAsnSerLeuPheAsnThrThrValVal 475
Db      1867 GAGTGGACCAAACTTCTGTGTATGTTCAGAAATGATTTATCAGAAATTAATACATATTT 1926
Qy      476 Tyr----- 476

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Db      1927 TATGAACCATCATTTGGAAATGAAACTGCTGTGAATGTGATTTCTCCACACAGAAATAT 1986
Qy      476 ----- 476
Db      1987 ACATTGCTCTTTAGTACTAGTACACATTTGATGATGATAGAAATGACAGATACACAGAT 2046
Qy      476 ----- 476
Db      2047 GAAGTGGAAAGATGTCCAGAAATTCATTTTACTACCCCAAGTTTGTCTCAAGAGAA 2106
Qy      476 ----- 476
Db      2107 ATTGAAGCCATAGTCTGCTGTTGTGCTTACATTTCTATGACAACTCTTCTGGAGTG 2166
Qy      477 -----IleProAsp 479
Db      2167 CTGTCTGCTTAAATGAAGAGACCTTAATTAACCAATCTGTGCTTAATGTTCCAGAT 2226
Qy      480 LeuAsnThrGlyTyrIleProGlnIleSer-----AsnPheLeu 492
Db      2227 CCTTCAAGAGATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2286
Qy      493 ProGluGlySerIleSerAsnAsnAsn-----GluIleThr 505
Db      2287 TCMAAGATCAAAATGATTCAGATGCGCATTTTCACTGATGATGATGATGATGATGAA 2346
Qy      506 SerLeuThrLeuIlePro-----ProValAsp-----SerLeuAsp----- 517
Db      2347 GCAATGACAAAAGCCTTTTCCAGAAAGATCTGAATTCATTTGACCTGTTCAAAAAGAA 2406
Qy      518 -----SerGlyAsnAsnProAsnGluIle 526
Db      2407 AAATTAATTAATGAGACACACAGCTGTATTTGGGGGCTTCAATGATGATCTTCT 2466
Qy      527 HisProAsnPheIlePheSerValSerSerValSerSerIleThrIlePheLeu 546
Db      2467 AGGCGACGATTTCTTACAGTATGAAATGAAATCTTCA---CAAAACCTTGAGACACT 2523
Qy      547 GlyIleLeuSerLeuIleLeuAsnGlnIle---GluCysSerSerProAspIleGln--- 554
Db      2524 GTCCAGATTTCTACCGTGTACACAGATGCTACACACCAAGTCTCGTACAGTCAAGTC 2583
Qy      565 AsnSerValGluGluGluThrThrMetLeuLeuGluAsnAspSerProSerGluThrIle 584
Db      2584 TTCTCAAGATCCAGTCTACCCAGCCCTGTGTAGAT-----TCAGAGAGCGG 2631
Qy      585 ProGluGlnThrLeuLeuProAspGluPheValSerCysLeuGlyIleValIleAsnGlu 604
Db      2632 CCAAGAGATCTTACAAATTAAGATCATGATGATGATGATGATGATGATGATGATGAT 2691
Qy      605 LeuProSerIleAsnThrTyrPheProGlnAsnIleLeuGlu----- 618
Db      2692 -----CAGTCTTCAACAGAACTGCAAGTACAGATTAATCCAGAT 2736
Qy      619 ---SerHisPheAsnArg 623
Db      2737 ATTTCACATTTTGAAGG 2754

RESULT 13
US-09-949-002-250
; Sequence 250, Application US/09949002
; Patent No. 690016
; GENERAL INFORMATION:
; APPLICANT: VENTUR, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823

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; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 250
; LENGTH: 3085
; TYPE: DNA
; ORGANISM: Human
; US-09-949-002-250

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## Alignment Scores:

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Pred. No.:      3,05e-12      Length:      3085
Score:          208.00        Matches:      172
Percent Similarity: 32.7%      Conservative: 118
Best Local Similarity: 19.4%      Mismatches: 276
Query Match:    6.3%          Indels:      320
DB:             3             Gaps:        44

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US-10-667-289-2 (1-629) x US-09-949-002-250 (1-3085)

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QY      4 ValThrIleGlnTrpAraAlaValIleAlaLeuTyrlleuPheSerTrpCysHleGly 23
DB      259 TTGACGTTGAGACCTTGCGTACAGCCCTGTTATTTTCCACGACGATCTACA 318
QY      24 GlyIleThrAsnIleAsnCySerGlyHisIleTrpValGluProAlaThrIlePheLys 43
DB      319 GGTGAAGCTTACATCCATGTT---GGTTATATCAGTCTGAA---TCTCCAGTTGTACA 372
QY      44 MetGlyMetAsnIleSerIleTyrcysGlnAlaAlaIleLysAsnCySglnProArgLys 63
DB      373 CTTCATCTTAATTTCACTGCGACGTTGT---GTGCTAAAGGAAAAATGATGATAT 426
QY      64 LeuHisPheTyrlYsaEngIlyle-----LysGlu 73
DB      427 TTTCATGTAATGCTATATCATTTGTCTGAGAAACAAACATTTACTATCTTAAGAG 486
QY      74 ArgPheGlnIleThrArgIleAsnLysThrAlaArgLeuTrpYrlYsaAsnPheLeu 93
DB      487 CAATATCTACTATC-----ATTAACAGAACAGCATCCAGTGTCACTTACAGATATAGCT 540
QY      94 GluProHisAlaSerMetYrcysThrAlaGluCyProLysHisPheGlnGluThrLeu 113
DB      541 TCATTAATTAATTCAGCTCAGCTTGCACATCTTACATTCGACAGCTTGAAACGAAAT-- 597
QY      114 IleCysGlyLysAspIleSerSerGlyTyrcProProAspIleProAspGluValThrCys 133
DB      598 GTTTATGAGATACAAATATTTCAAGCTTGCCTCCAAAAAACCTAAATTTGAAGTGC 657
QY      134 ValIleTyrcGluTyrcSerGlyAsnMetThrCysThrTrpAsnAla**LysLeuThrTyrc 153
DB      658 ATGTGTAACGAG---GGGAGAGAAATGAGGTGTGAGGTGAGTGTGAGAGGAAACACAC 714
QY      154 IleAspThrIlyserYrValValHis----- 161
DB      715 TTGGAGCAAACTTCACTTAATAATCTGAATGGGCAACACAAAGTTGCTGATTCGAAA 774
QY      162 ---ValLysSerLeuGlnTrpGlnGluGlnGlnIleuThrSerSerTyrlleAsn 180
DB      775 GCAAAACGTACACCCCACTCAGTCAGCTTGATTAATTTCTACTGTGTATTTTGTCAC 834
QY      181 IleSerThrAspSerLeuGlnGlyLysLeuTyrcValIleTrpValGlnAlaIleAsn 200
DB      835 ATTGAA-----GTCTGGGTAGAGAGAGAGAAAT 861
QY      201 AlaLeuGlyMetGluSerLysGlnLeuGlnIleHisLeuAspIleVal----- 218
DB      862 GCCCTTGGAGAGTTACATCAGAT---CATATCAATTTTATATCTGATTAATAAGTG 915
QY      219 -----IleProSerAlaAlaValIleSerArgIleGluThrIleAsnAlaThrVal 235
DB      916 AAGCCCAATCGCGCAATATTTATATGATCACTACACAGAGAACTGTGATATCTTA 975
QY      236 ProLysThrIleIleTyrcTrpAspSerGlnThr-----ThrIleGluLysValSerCys 253
DB      976 AATATGCA-----TGGACCAACCCAAAGTATTAAAGGTATTATTAATTAATAATAT 1026

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QY      254 GluMetArgTyrlYsaValaThrThrAsnGlnThrTrpAsn---ValLysGluPheAspThr 272
DB      1027 AACATTCAATATATGAGACCAAGATGCGCTCAACTTGGAGCCAGATTTCTCTGGAAGACA 1086
QY      273 AsnPheThrTyrcValGlnInsSerGluPheTyrcLeuGluProAsnIleLysTyrcValPhe 292
DB      1087 GCATCCACCCGATCTTCATTCACGTGCCAAGACCTTAACCTTTTACAGATATATGTGTT 1146
QY      293 GlnValArgCys---GlnGluThrGlyLysArgTyrcTrpGlnProTrpSerSer----- 309
DB      1147 AGGATTCGCTGTATGAGAAAGATGTGAAGGATACGTAGTGACTGAGTGAAGAAACA 1206
QY      310 -----ProPhePheIlyserThrPro 316
DB      1207 AGTGGATCACCTATGAAAGATAGACATTAAGCAACCAAGTTCTTGTTAAATAGAT 1266
QY      317 -----GluThrValPro----- 320
DB      1267 CCATCCCATCTCAAGCTACAGAACTGTACAACTCGTGTGAAAGACATTCCTCTTTT 1326
QY      321 GlnValThrSerLysAlaPheGlnHisAspThr-----TrpAsnSerGlyLeu 336
DB      1327 GAAGCCCAATGGAATAATCTTGATTAAGAGTGACTCTCAACAGATGAATACATTTA 1386
QY      337 -----ThrVal---AlaSerIleSerThrGlyHisLeuThrSerAspAsnArgGly 352
DB      1387 CAATAATACACATTAATGTCACAAATGCAAGTAAATCTCAATAATGATCCG----- 1440
QY      353 AspIleGlyLeuLeuLeuGlyMetIleValPheAlaValMetLeuSerIleLeuSerLeu 372
DB      1441 -----TATCTAGCAACCTTAACAGTAAGAAATCTT 1470
QY      373 IleGlyIlePheAsn----- 377
DB      1471 GTTGGCAATACAGATCAGCTGTTTAATCAATCCCTGCTGATCTTCAAGTACTCAC 1530
QY      378 -----ArgSerPhe----- 380
DB      1531 CCTGTATGAGATTTTAAGATTCCTCCCAAGATTAACATGCTTGGGTGGAATGAGACTACT 1590
QY      381 ---ArgThrGlyIleLysArgArgIleLeuLeuLeuIleProLysTrpLeuTyrcGluAsp 399
DB      1591 CCAAGGAATCTGTAAAGAAATATATATCTT---GAGTGTGT----- 1629
QY      400 IleProAsnMetLysAsnSerAsnValValLysMetLeuGlnGluAsnSerGluLeu--- 418
DB      1630 GNGTTATCAGATTAACACCCCTGTATCACAGCTGCCAACAGAAAGATGTGTACCGTGCAT 1689
QY      419 -----MetAsnAsnAsnSerSerGlnGlnValLeuTyrc-----ValAspPro 432
DB      1690 CGCACTATTTTAAGAGAGAACTTAGCAGAGAGCAAAATGCTATTTGATTAACAGTTACTCCA 1749
QY      433 MetIleThrGlu-----IleLysGluIlePhe 441
DB      1750 GATATGATCGATGAGACAGAGACCTGATATCCATTAAGCATATACCTTAACAAGCT--- 1806
QY      442 IleProGlnHisLysProThrAspTyrcLysLys-----GluAsnThrGlyProLeu 458
DB      1807 CCACCTTCCAAAGACACTTCTGTTCGACAAAAAAGTAGGAAAAAGCAAGCTGTCTTTA 1866
QY      459 GluThrArgAspTyrcPro-----GlnAsnSerLeuPheAspAsnThrThrValVal 475
DB      1867 GAGTGGAGACCACTTCTGTGTATGTTTCAGATGATATTAACAAATTAATTAATATTTT 1926
QY      476 TYT----- 476
DB      1927 TATAGAACATCATCTGGAATGAATGAACTGCTGATGATGGAATCTTCCACACAGATAT 1986
QY      476 ----- 476
DB      1987 ACATGTCTCTTTGACTATGATGACACATTTGATGATGATGCAATGTCAGATACAGAT 2046
QY      476 ----- 476

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Db      2047 GAAGTGGAGAGATGTCAGCAATTCATTCTTACTACCCCAAGTTTCTCAAGAGAA 2106
Qy      476 -----
Db      2107 ATTGAAGCATTAGTCGTCCTGTTGCTTACGATTCCTATTGACAACTCTTCTGGAGTG 2166
Qy      477 -----
Db      2167 CTGTTCTGCTTATAAAGCAGACCTAATTAATAAACATCTGGCTTAATGTTCCAGAT 2226
Qy      480 LeuasnThiGlyTyrIysProGlnIleSer-----AsnPhelu 492
Db      2227 CCTTCAAGAGTCATATGCGCCAGTGCTCACCTCACACTCTCCAGCACAATTTTAAT 2286
Qy      493 ProGlnGlySerHisLeuSerAsnAsnAsn-----GluIleThr 505
Db      2287 TCAAAAGATCAAAATGATTAATTCAGATGGCAATTTCACTGATGTAAGTGTGGAATTAAGAA 2346
Qy      506 SerLeuThrLeuIysPro-----ProValAsp-----SerLeuAsp----- 517
Db      2347 GCAATGACAAAAGCCTTTTCCAGAAAGATCTGAATCATTTGACCTGTTCAAAAGGAA 2406
Qy      518 -----
Db      2407 AAATTAATACTGAGAGACACAGCAGTGTATTTGGGGGCTTCATGTCATGTCATCTTCT 2466
Qy      527 HisProAsnPhelAlaPheSerValSerSerValAsnSerLeuSerAsnThriIlePhelu 546
Db      2467 AGGCACAGCATTTCTGACAGTGAATGAATGAATCTTCA---CAAAACCTTGGAGCACT 2523
Qy      547 GlyIleLeuSerLeuIleLeuAsnGlnGly---GluCysSerSerProAspIleGln--- 564
Db      2524 GTCCAGATTTCTACCGGTGATACACAGTGGCTACAGACACCAAGTCCGTGATCCCAAGTC 2583
Qy      565 AsnSerValIleGlnGluIleThrMetLeuLeuGlnAsnAspSerProSerGluThrIle 584
Db      2584 TTCTCAGATCCAGTCTACCCAGCCCTGTGTAGAT-----TCAGAGAGCGG 2631
Qy      585 ProGlnGlnThiLeuLeuProAspGluPheValSerCysLeuGlyIleValAsnGlnGlu 604
Db      2632 CCGAAGATCTTACATTAATGATCATGTGATGATGCGGTGATATTTGCCAGGCAA 2691
Qy      605 LeuProSerIleAsnThriTyrPheProGlnAsnIleLeuGlu----- 618
Db      2692 -----CAGTACTTCAACAGACAGACGTCAGTCAGATGAATCCAGTCAGAT 2736
Qy      619 ---SerHisPheAsnArg 623
Db      2737 ATTTCACATTTTGAAAG 2754

RESULT 14
US-08-825-558-3
; Sequence 3, Application US/08825558
; Patent No. 5965724
; GENERAL INFORMATION:
; APPLICANT: SHARKEY, ANDREW
; APPLICANT: SMITH, STEPHEN K.
; APPLICANT: DELLOW, KIMBERLEY A.
; TITLE OF INVENTION: GP 130 Lacking the Transmembrane Domain
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,558
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0623,0530001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1977 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1974
; US-08-825-558-3

Alignment Scores:
Pred. No.: 1,86e-12 Length: 1977
Score: 207.00 Matches: 124
Percent Similarity: 36.8% Conservative: 97
Best Local Similarity: 20.6% Mismatches: 208
Query Match: 6.2% Indels: 172
Db: 2 Gaps: 32

US-10-667-289-2 (1-629) x US-08-825-558-3 (1-1977)
Qy      4 ValThrIleGlnThrAspAlaValIleAlaLeuTyrIleLeuPheSerTyrCysHisGly 23
Db      4 TTACCGTTGACGACTTGGGATGTCAGAGCCTTGTATTTCTCTCCACCTGAATATCA 63
Qy      24 GlyIleThrAsnIleAsnCysSerGlyHisIleThrValGluProAlaThrIlePheIys 43
Db      64 GGTGAATCTTACATCATCATGT---GGTATATCAGTCTGAA---TCTCAGATTGACAA 117
Qy      44 MetGlyMetAsnIleSerIleTyrCysGlnAlaIleIleIysAsnGlySerGlnProAspGly 63
Db      118 CTTCATCTTAATTTCACTGCACTGTGTGT---GTCTAAAGGAAAATGTATGATTA 171
Qy      64 LeuHisPheTyrIysAsnGlyIle-----LysGlu 73
Db      172 TTTCATGTAATGCTTAATTAATGATGTCGAAAACAACATTTTACTATCTTAAGAG 231
Qy      74 ArgPheGlnIleThrArgIleAsnIysThrThrAlaArgLeuTyrTyrIysAsnPhelu 93
Db      232 CAATATATCATC-----ATTAACAGAACGATCAGATCCAGTTCACATTAAGATTA 285
Qy      94 GluProHisAlaSerMetTyrCysThrAlaGluCysProIysHisPheGlnGluThrLeu 113
Db      286 TCATTAAATATTCAGCTCACTTGCACCAATTTCTTACATTCGAGACAGCTTGAAACGAAT-- 342
Qy      114 IleCysGlyIysAsnIleSerSerGlyTyrProProAspIleProAspGluValThrCys 133
Db      343 GTTATGAAATTCACATTAATTAATGATGAGCTTCCCGAAGAAAACCTTAATTTGAATGC 402
Qy      134 ValIleTyrGlnTyrSerGlyAsnMetThrCysThrTrpAsnAla**LysLeuThrTyr 153
Db      403 ATGTGAAGAG---GGAAAGAAATGAGGTGAGTGGAGTGGTGAAGGAAACACAC 459
Qy      154 IleAspThrIysTyrValIleHis----- 161
Db      460 TTGAGACAAACTTCACTTAATAATCTGAATGGCAACACACAACTTGTGATTCGAAA 519
Qy      162 ---ValIysSerLeuGluThrGlnGlnGlnIleTyrIleThrSerSerTyrIleAsn 180
Db      520 GCAAAAGTGAACACCCCACTGATGACCTGTTGATTAATTTCTAGTGTATTTGTGCAC 579

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Qy 181 ILeSerThraSerLeuGlnGlyLysLeuValTrrValGlnAlaAlaAsn 200
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Db 580 ATTGAA-----GTCGGGATGAAGCAGAAAT 606
Qy 201 AlaLeuGlyMetGluSerLysGlnLeuGlnIleHISLeuAspAlaVal----- 218
    |||
Db 607 GCCCTGGGAAGGTATACATAGAT-----CATATCAATTTTGTCTCTGATATATAAGTG 660
Qy 219 -----IleProSerAlaAlaValIleSerArgAlaGluThrIleAsnAlaThrVal 235
    |||
Db 661 AAGCCCAATCCGCAATTAATTTATCATGATACATCAAGAGCAAGCTCTAGATCTTA 720
Qy 236 ProLeuThrIleLeuTrrTrpAspSerGlnThr-----ThrIleGluLysValSerCys 253
    |||
Db 721 AATTTGCA-----TGACCAACCAAGTATTAAAGTGTATTAATACTAAATAT 771
Qy 254 GluMetArgTrrLysAlaThrThrAsnGlnThrTrpAsn-----ValLysGluPheAspThr 272
    |||
Db 772 AACATTCATATAGACCAAAAGATGCTCAACTGGAGCAGATTCCTCTGAAGACACA 831
Qy 273 AsnPheThrTrrValGlnGlnSerGluPheTrrLeuGluProAsnIleLysTrrValPhe 292
    |||
Db 832 GCATCCACCCGATCTTCAATTCATGTCACAGACCTTAACCTTTTACAGAAATATGTTT 891
Qy 293 GlnValArgCys--GlnGluThrGlyLysArgTrrTrrGlnProTrrPserSer----- 309
    |||
Db 892 AGGATTCGCTGTATGAAGAGATGATGATAGGATACCTGAGATCACTGATGAAGAAGCA 951
Qy 310 -----ProPhePheHISLysTrrPro 316
    |||
Db 952 AGTGGATCACTATGAAGATAGACATTAAGACCAAGTTTCTGTATTAATAATAGAT 1011
Qy 317 -----GluThrValPro----- 320
    |||
Db 1012 CCATCCCAATCTCAGAGCTACAGAACTGTACAACCTGTCGAGAGACATTCCTCTTTT 1071
Qy 321 GlnValThrSerLysAlaPheGlnHISAspThr-----TrrAsnSerGlyLeu 336
    |||
Db 1072 GAAGCCATGAGAAAATCTTGATTAAGAGTACCTCACAAGATGGAATCATCTTA 1131
Qy 337 -----ThrVal--AlaSerIleSerThrGlyHISLeuThrSerAspAsnArgGly 352
    |||
Db 1132 CAATAATTACACAGTATATGCCACAAACTGACAGTAAATCTCACAATAATGATCGC----- 1185
Qy 353 AspIleGlyLeuLeuGlnMetIleValPheAlaValMetLeuSerIleLeuSerLeu 372
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Db 1186 -----TATCTACCAACCTTAACAGTAAGAAATCTT 1215
Qy 373 IleGlyIlePheAsn----- 377
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Db 1216 GTTGGCAATTCAGATGCACTTTTAATCTCCCTGCTGTGACTTTCAAGCTACTCAC 1275
Qy 378 -----ArgSerPhe----- 380
    |||
Db 1276 CCGTATATGATCTTAAGCATTCCTCCAAAGATTAACATGCTTTGGGTGAATGAGACTACT 1335
Qy 381 --ArgThrGlyIleLysArgGlnIleLeuLeuIleProLysTrrPLeuTrrGluAsp 399
    |||
Db 1336 CCAAGGGAATCTCTGAAGAAATATATATCTT-----GAGTGTGT----- 1374
Qy 400 IleProAsnMetLysAsnSerAsnValValLysMetLeuGlnGluAsnSerGluLeu-- 418
    |||
Db 1375 GTGTATCATAGATAAGCACTGTATACAGACTGGCAACAGAAAGTGTACCGTGCAT 1434
Qy 419 -----MetAsnAsnAsnSerSerGluGlnValLeuTrr-----ValAspPro 432
    |||
Db 1435 CGCACTATTTAAGAGGAACTTACAGAGAGCAAAATGATTTGATTAACAGTTACTCA 1494
Qy 433 MetIleThrLys-----IleLysGluIlePhe 441
    |||
Db 1495 GTATATGCTATGACCAAGAGCCCTGAATTCATTAAGCAATACCTTAACAGCT-- 1551
Qy 442 IleProGluHISLysProThrAspTrrLysLys-----GluAsnThrGlyProLeu 458

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Db 1552 CCACCTTCCAAAGCACTACTGTTCGACAAAAAGTAGCAAAAAAGAGCTGTCTTA 1611
Qy 459 GluThrArgAspTrrPro-----GlnAsnSerLeuPheAsnThrThrVal 475
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Db 1612 GAGTGGACCAACTTCTCTGTGATGTTCAGAAATGATTTATCAGAAATTAATAATATTT 1671
Qy 476 Tyr 476
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Db 1672 TAT 1674

RESULT 15
US-09-312-611-3
; Sequence 3, Application US/09312611
; Patent No. 6380160
GENERAL INFORMATION:
APPLICANT: SHARKEY, ANDREW
APPLICANT: SMITH, STEPHEN K.
APPLICANT: DELLOW, KIMBERLEY A.
TITLE OF INVENTION: GP130 Lacking the Transmembrane Domain
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/312,611
FILING DATE: 17-MAY-1999
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0623.0530002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1977 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1974
US-09-312-611-3

Alignment Scores:
Pred. No.: 1.86e-12 Length: 1977
Score: 207.00 Matches: 124
Percent Similarity: 36.8% Conservative: 97
Best Local Similarity: 20.6% Mismatches: 208
Query Match: 6.2% Indels: 172
Gaps: 32

US-10-667-289-2 (1-629) x US-09-312-611-3 (1-1977)
Qy 4 ValThrIleGlnThrAspAlaValIleAlaLeuTrrIleLeuPheSerTrrCysHISGly 23
    |||
Db 4 TTAGCGTTCAGACCTTGGGATGCAAGCTTGTATTTCTCTCACTCACTGAATGATCA 63
Qy 24 GlyIleThrAsnIleAsnCysSerGlyHISIleTrrValGluProAlaThrIlePheLys 43
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Db 64 GGTGAACCTTCTAGATCCATGT--GGTATATCATGTCCTGA--TCTCCAGTTGTACAA 117

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QY 44 MetGlyMetAsnIleSerIleTyrCysGlnAlaIleIleYsAsnCysGlnProArgLys 63
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QY 64 LeuHisPheTyrIleAsnGlyIle-----LysGlu 73
Db 172 TTTCAATTAATATGCTAATTATCATTTGTCTGAAAAAACAATTTTACTATTCTTAAGAG 231
QY 74 ArgPheGlnIleThrArgIleAsnIleThrAlaArgLeuTyrIleYsAsnPheLeu 93
Db 232 CATATATCTATC-----ATPAACAGAAACGATCCAGTGCATCTTACAGATATAGCT 265
QY 94 GluProHisAlaSerMetTyrCysThrAlaGluCysProIleHisPheGlnIleThrLeu 113
Db 286 TCATTAATATATTCAGCTCAGCTGCACATTCCTTACATTCGAGACGTTGAACAGAAAT--- 342
QY 114 IleCysGlyIleYsAsnIleSerSerGlyTyrProProAsnIleProAsnGlyIleThrCys 133
Db 343 GTTATATGGAATCAACAATTAATTTTCAGGCTTCCTCAAAAAAATTAAGAGTTGC 402
QY 134 ValIleTyrGluTyrSerGlyAsnMetThrCysThrTrpAsnAla**LysLeuThrTyr 153
Db 403 ATTGTGAACAG---GGGAAAAAATGAGGTGTGAGTGGATGTGTGAAGGAAACAC 459
QY 154 IleAspThrIleTyrValIleHis----- 161
Db 460 TTGGAGACAAACTTCACCTTAATAATCGAATGGGCAACACAAAGTTGCTGATTCGAAA 519
QY 162 ---ValIleSerLeuGluThrGluGluGlnGlnIleTyrLeuThrSerSerTyrIleAsn 180
Db 520 GCAAAAGATGACACCCCTCCTGATGATGATTAATCTGATGATTTGTTGTAAC 579
QY 181 IleSerThrAspSerLeuGlnGlyIleYsIleTyrLeuValIleTrpValGlnAlaIleAsn 200
Db 580 ATTGA-----GCTGGGTAAGACGAGAAAT 606
QY 201 AlaLeuGlyMetGluSerIleGlnLeuGlnIleHisIleuAspAspIleVal----- 218
Db 607 GCCCTGGAGAGTTACATCAGAT-----CATATCAATTTTGTATCTGTATATTAAGTG 660
QY 219 -----IleProSerAlaIleValIleSerArgIleGluThrIleAsnAlaIleThrVal 235
Db 661 AAGCCCAATCCGACCATTAATTTATCATGATCAACAGAGAACTGTGTAGATCTTA 720
QY 236 ProIleThrIleIleTyrTrpAspSerGlnThr-----ThrIleGluIleValSerCys 253
Db 721 AATTTGACA-----TGACCAACCCAGATTAAGAGTGTATTAATTAATTAATAT 771
QY 254 GluMetArgTyrIleValAlaThrThrAsnGlnThrTrpAsn---ValIleGluPheAspThr 272
Db 772 AACATTCATATATAGACCAAAAGATGCTCAACTGGAGCCAGATTCTCTCGAAAGACACA 831
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Db 832 GCATCCACCCGATCTTCATTCATCTGTCCAAAGACCTTAACCTTTTACAGAAATATGTGTT 891
QY 293 GlnValArgCys---GlnGluThrGlyIleYsArgTyrTrpGlnProTrpSerSer----- 309
Db 892 AGGATTCGCTGTATGAAGAAAGATGTAAAGGATATCTGAGTGAAGTGAAGAAAGCA 951
QY 310 -----ProPhePheHisIleYsThrPro 316
Db 952 AGTGGATCACTATGAAGATAGACATTAAGACCAAGATTTCTGGTATTAATAATAGAT 1011
QY 317 -----GluThrValPro----- 320
Db 1012 CCATCCCATACTCAAGGCTACAGAACTGTACACTGTGTGAGACATGCTCTCTTT 1071
QY 321 GlnValThrSerIleYsAlaPheGlnHisAspThr-----TrpAsnSerGlyIleu 336
Db 1072 GAAGCCAAATGAAAAATCTTGATTAATGAAGTGACTCTCACAGATGAATCAATTTA 1131

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QY 337 -----ThrVal---AlaSerIleSerThrGlyHisLeuThrSerAspAsnArgGly 352
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QY 353 AspIleGlyIleuLeuLeuGlyMetIleValIlePheAlaValMetLeuSerIleLeuSerLeu 372
Db 1186 -----TATCTAGCAACCTTAACAGTAAGAAATCTT 1215
QY 373 IleGlyIlePheAsn----- 377
Db 1216 GTTGGCAAAATCAGATGACAGCTGTTTAAGTATCTCTGCTGTGACTTCAAGTACTAC 1275
QY 378 -----ArgSerPhe----- 380
Db 1276 CCTGTATATGATCTTTAAAGCATTCGCCAAAGATPAACATGCTTTGGTGGATGAGTACT 1335
QY 381 ---ArgThrGlyIleIleYsArgIleLeuLeuLeuIleProIleThrLeuTyrGluAsp 399
Db 1336 CCAAGGGAATCTGTAAAGAAATATATATCTT-----GAGTGTGT----- 1374
QY 400 IleProAsnMetIleYsAsnSerAsnValIleYsMetLeuGlnIleuAsnSerGluLeu--- 418
Db 1375 GTGTTATCAGATTAAGACACCTGTATCACAGACTGGCAACAAAGATGTGTACCGTCAAT 1434
QY 419 -----MetAsnAsnAsnSerSerGluGlnValIleuTyr-----ValAspPro 432
Db 1435 CGCACTTATTTAAGAGGAATCTTAGCAGAGAGCAATGCTATTTGATTAACAGTACTTCA 1494
QY 433 MetIleThrGlu-----IleYsGluIlePhe 441
Db 1495 GTTATATGCTATGAGACAGAGAACCTTGAAATCATTAAGCATACCTTAACAAAGCT--- 1551
QY 442 IleProGluHisIleYsProThrAspTyrIleYs---GluAsnThrGlyProLeu 458
Db 1552 CCACCTTCCAAAGACCTACTGTTCGACAAAAAAGTAGGAAAAACGAAGCTGTCTTA 1611
QY 459 GluThrArgAspTyrPro-----GlnAsnSerLeuPheAspAsnThrThrValVal 475
Db 1612 GAGTGGAGACCAACTCTGTGTGATGTTCAGAAATGATTAATCAGAAATTAATTAATTTT 1671
QY 476 Tyr 476
Db 1672 TAT 1674

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Search completed: October 14, 2006, 14:50:05  
Job time : 360 secs